

Jarrell, Noble

181606

From: Ramirez, Delia
Sent: Tuesday, March 07, 2006 5:49 PM
To: Jarrell, Noble
Subject: 09/541,462

Hi,

I would like to request the following search:

1. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases (commercial only)

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Noble

Fin 3/16/06

4 NA oligo

20Prn compugser

20000

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Jarrell, Noble

From: Ramirez, Delia
Sent: Tuesday, March 07, 2006 5:44 PM
To: Jarrell, Noble
Subject: 09/541,462

Hi,

I would like to request the following INTERFERENCE search:

1. SEQ ID NO:1 and 2 in the nucleic acid databases.
2. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 09:47:22 ; Search time 530 Seconds
(without alignments)
470.166 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 108
Sequence: 1 MAAMVDVTFSTGNSGAGK.....KTRQVCPLDNREWFQYKH 108

Scoring table:
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 115364844 residues
Word size: 12

Total number of hits satisfying chosen parameters: 12
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	74	68.5	660	9 US-11-096-568A-11809	Sequence 11809, A
2	70	64.8	432	9 US-11-096-568A-14405	Sequence 14405, A
3	42	38.9	693	9 US-11-096-568A-26820	Sequence 26820, A
4	40	37.0	348	9 US-11-096-568A-28569	Sequence 28569, A

C	5	12	11.1	153	7	US-10-932-182A-81177	Sequence 81177, A
C	6	12	11.1	153	7	US-10-932-182A-81177	Sequence 81177, A
C	7	12	11.1	207	7	US-10-932-182A-6146	Sequence 6146, Ap
C	8	12	11.1	207	7	US-10-932-182A-6146	Sequence 6146, Ap
	9	12	11.1	366	7	US-10-932-182A-2279	Sequence 2279, Ap
	10	12	11.1	366	7	US-10-932-182A-78459	Sequence 78459, A
	11	12	11.1	366	7	US-10-932-182A-2279	Sequence 2279, Ap
	12	12	11.1	366	7	US-10-932-182A-78459	Sequence 78459, A

ALIGNMENTS

RESULT 1
US-11-096-568A-11809
; Sequence 11809, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11809
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 13657464
US-11-096-568A-11809

Alignment Scores:
Pred. No.: 1.49e-71 Length: 660
Score: 74.00 Matches: 74
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 68.5% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-11809 (1-660)

Qy	25	LVSLYSTPAsnAlaValAlaLeuTTPAlaTTPAspIleValValAspAsnCysAlaTlle	44
Db	208	AAGAAGTGAACGCCGCTCTGGCGTGGGACATCGTGGTGGACAACTGGCCCATC	267
Qy	45	CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr	64
Db	268	TGCCGTAAACACATCATGGATTATGATCGAGTCCAGCCCAACAGGCCAGGCCACC	327
Qy	65	SerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHisCysIle	84
Db	328	AGCGAGGAGTGCACCGTCGCATCGGCTGTCTGTAAATCATGCTTCCACTTCCACTGCATC	387
Qy	85	SerArgTTPLeuLysThrArgGlnValCysProteinAspAsn	98
Db	388	AGCAGGTGGCTCAAGACTCGCCCAAGTGTGCCCACTAGACAAC	429

RESULT 2

US-11-096-568A-14405
; Sequence 14405, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14405

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; LENGTH: 432
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(432)
; OTHER INFORMATION: Ceres Seq. ID no. 4776740
US-11-096-568A-14405

Alignment Scores:
Pred. No.: 2,64e-67 Length: 432
Score: 70.00 Matches: 70
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 64.8% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-14405 (1-432)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHis 48
Db 188 GCGGTGCTCTCTGGGCTTGGGATATCGTTGTTGACAAATTCGGCCATCTGCAGAAACAC 247
Qy 49 IleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCys 68
Db 248 ATCATGGATCTCTGTATTGAATGTCAGGCTAATCAGCCGCGCTACGAGTGAGGAATGC 307
Qy 69 ThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeu 88
Db 308 ACTGTTGCTTGGGGGGTTTGCATCAGCCCTTCACCTTCCTGCTCATCAGCAGATGTTA 367
Qy 89 LysThrArgGlnValCysProLeuAspAsn 98
Db 368 AAGACTCGTCAAGTTGCCCATTCGATAAC 397

RESULT 3
US-11-096-568A-26820
; Sequence 26820, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26820
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(693)
; OTHER INFORMATION: Ceres Seq. ID no. 13622871
US-11-096-568A-26820

Alignment Scores:
Pred. No.: 2,29e-36 Length: 693
Score: 42.00 Matches: 42
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 38.9% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-26820 (1-693)

Qy 32 LeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAsp 51
Db 207 CTCCTGGGCTGGACATCGTGGTGACAACTTCGGCCATCTGCCGCAACCATCATGAGAC 266
Qy 52 LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla 71
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Db 267 CTTTGCATCGAGTGCAGGCGCAACACGAGCGCGCCACCGAGGAGTGACACCGTCGCT 326
Qy 72 TrpGly 73
Db 327 TGGGGA 332

RESULT 4
US-11-096-568A-28569
; Sequence 28569, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28569
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(348)
; OTHER INFORMATION: Ceres Seq. ID no. 3017472
US-11-096-568A-28569

Alignment Scores:
Pred. No.: 2,07e-34 Length: 348
Score: 40.00 Matches: 68
Percent Similarity: 97.1% Conservative: 0
Best Local Similarity: 97.1% Mismatches: 1
Query Match: 37.0% Indels: 2
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-28569 (1-348)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHis 48
Db 106 GCTGTGCTCTCTGGGCTTGGGATATCGTTGTTGATAACTGCGCAATTTGTAGGAATCAC 165
Qy 49 IleMetAspLeuCysIleGluCysGln-AlaAsnGlnAlaSerAlaThrSerGluGluCys 68
Db 166 ATCATGGATCTCTGTATTGAATGCT-AGCTATCAGCTAGTCCCTAGTAGGAATG 224
Qy 68 sThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLe 88
Db 225 CACTGTTGCTTGGGGGGTTTGCAACCAACGCTTTCCTTCCTGCTATCAGCAGATGGCT 284
Qy 88 uLysThrArgGlnValCysProLeuAsp 97
Db 285 CAAAACTCGTCAAGTGTGTCCACTAGAT 312

RESULT 5
US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 81177
; LENGTH: 153
; TYPE: DNA
```

ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81177

Alignment Scores:
Pred. No.: 0.000629 Length: 153
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 68 GTTGACAACTGTGCTATTTCAGGAAACCATATAATG 33

RESULT 6

US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81177
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81177

Alignment Scores:
Pred. No.: 0.000629 Length: 153
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 68 GTTGACAACTGTGCTATTTCAGGAAACCATATAATG 33

RESULT 7

US-10-932-182A-6146/c
; Sequence 6146, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6146
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-6146

Alignment Scores:
Pred. No.: 0.000804 Length: 207
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 47 GTTGACAACTGTGCTATTTCAGGAAACCATATTATG 12

RESULT 8

US-10-932-182A-6146/c
; Sequence 6146, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6146
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-6146

Alignment Scores:
Pred. No.: 0.000804 Length: 207
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 47 GTTGACAACTGTGCTATTTCAGGAAACCATATTATG 12

RESULT 9

US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

Qy 39 ValaspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTATTTCAGAGAACCATATG 189

RESULT 10

US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 39 ValaspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTATTTCAGAGAACCATATG 189

RESULT 11

US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

Qy 39 ValaspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTATTTCAGAGAACCATATG 189

RESULT 12

US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 39 ValaspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTATTTCAGAGAACCATATG 189

Search completed: March 11, 2006, 12:07:37
Job time : 531 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:24:33 ; Search time 653 Seconds
(without alignments)
1367.677 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 MAAMVDVTPSGTNGAGKK.....KTRQVCLDNRWEFKYGH 108

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA_Main -QFMT=fastcap -SUFFIX=rnpsbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Database : Published Applications NA_Main:

1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	433	7	US-10-242-535A-43377
2	616	100.0	433	7	US-10-085-783A-43377
3	616	100.0	453	7	US-10-242-535A-35025
4	616	100.0	453	7	US-10-085-783A-35025
5	616	100.0	467	7	US-10-242-535A-39933
6	616	100.0	467	7	US-10-085-783A-39933
7	616	100.0	471	7	US-10-242-535A-57254

8	616	100.0	471	7	US-10-085-783A-57254
9	616	100.0	472	7	US-10-242-535A-56068
10	616	100.0	472	7	US-10-085-783A-56068
11	616	100.0	504	8	US-10-913-937-5
12	616	100.0	508	8	US-10-913-937-3
13	616	100.0	523	7	US-10-242-535A-46292
14	616	100.0	523	7	US-10-085-783A-46292
15	611	99.2	476	3	US-09-918-995-17191
16	607	98.5	4543	5	US-10-198-846-11311
17	603	97.9	430	7	US-10-242-535A-54751
18	603	97.9	430	7	US-10-085-783A-54751
19	596	96.8	380	3	US-09-960-352-45675
20	586	95.1	4476	8	US-10-357-930-25604
21	573	93.0	5347	6	US-10-240-965-99
22	554	89.9	3484	8	US-10-723-860-1383
23	554	89.9	3484	9	US-10-756-149-1357
24	554	89.9	5111	5	US-10-205-823-382
25	554	89.9	5111	10	US-11-051-454-382
26	554	89.9	5371	8	US-10-723-860-5852
27	545	88.5	468	7	US-10-242-535A-47656
28	545	88.5	468	7	US-10-085-783A-47656
29	535	86.9	692	10	US-11-097-143-31031
30	524	85.1	840	7	US-10-767-701-12172
31	523.5	85.0	527	9	US-10-487-901-4266
32	523.5	85.0	531	9	US-10-487-901-4271
33	523.5	85.0	586	9	US-10-487-901-4270
34	523.5	85.0	617	9	US-10-487-901-4265
35	523.5	85.0	691	9	US-10-487-901-4263
36	523.5	85.0	1259	7	US-10-437-963-11395
37	522.5	84.8	619	7	US-10-425-114-25647
38	521	84.6	683	9	US-10-487-901-4262
39	520	84.4	673	9	US-10-487-901-4261
40	519.5	84.3	553	7	US-10-021-323-10545
41	519.5	84.3	608	8	US-10-767-795-687
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43	515.5	83.7	390	3	US-08-770-791-20
44	515.5	83.7	893	3	US-10-425-115-16831
45	514.5	83.5	544	8	US-10-767-795-688

ALIGNMENTS

RESULT 1

US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA

US-10-242-535A-43377
; ORGANISM: Human

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Pred. No.: 2.71e-74 Length: 433
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0


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; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-46292

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Best Local Similarity:	100.0%	Mismatches:
Query Match:	100.0%	Indels:
DB:	7	Gaps:

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19	ATGGCGGCGAGCGCATGGATGGATACCCGAGCGCCACCAACAGCGCGCGGCAAGAG	78
21	ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
79	CGCTTTGAAGTGAAAAAGTGGAAATGCGAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT	138
41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
139	AACTGTGCATCTCGAGGAACCAATTATGATCTTTGCATAGATGTCAAGCTAACCCAG	198
61	AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis	80
199	GGGTCCGTACTTTCAGAGAGTGTACTGTCCATGGGGAGTCTGTAAACATGCTTTTCAC	258
81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
259	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACAACACAGAG	318
101	TrpGluPheGlnLysTyrGlyHis	108
319	TGGGAAATTCAAAAGTATGGGCAC	342

RESULT 14

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US-10-085-783A-46292
; Sequence 46292, Application US/10085783A
; Publication NO. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-46292

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Alignment Scores:	
Pred. No.:	3,529-74
Score:	616.00
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Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	7
Length:	523
Matches:	108
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

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Qy	21	ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	79	CGCTTTGAAGTGAAGAAGTGGAAATGCAAGTAGCCCTCTGGCGCTCGGGAATATTGTGGTTGAT	138
Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	139	AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG	198
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	199	GCGTCCGCTACTTCAGNAGAGTGTACTGTGCATGGGGAGTCTGTACCATGCTTTTTCAC	258
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	259	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCTCCATTGGACAACAGACAG	318
Qy	101	TrpGluPheGlnLysTyrGlyHis	108
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RESULT 15

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US-09-918-995-17191
; Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17191

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Alignment Scores:	1.5e-73	Length:	476
Pred. No.:	611.00	Matches:	107
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	99.2%	Indels:	0
Query Match:	3	Gaps:	0
DB:	3		

US-09-541-462B-2 (1-108) X US-09-918-995-17191 (1-476)

Qy	2	AláAalaMetAspValAspThrProSerGlyThrAsnSerClyAlaGlyLysLysArg	21
Db	75	GCGGCAGCATGGATGTGGATACCCCGAGCGGCACCACAGCGCGCGGGCAAGAAGCGC	134

US-09-541-462B-2 (1-108) x C0698451 (1-433)

US-09-541-462B-2 (1-108) x AFL42059 (1-327)

JOURNAL Patent: WO 02070737-A 35025 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity: 100.0%  Mismatches: 0
Query Match: 100.0%  Indels: 0
DB: 6  Gaps: 0

US-09-541-462B-2 (1-108) x CQ690099 (1-453)

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QY
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DP

Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 84 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 143
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValIleGluCysGlnAlaAsnGln 60
 Db 144 AACTGTGCCATCTCGAGAACCAATTATGGATCTTTGCATAGAAATGTCAGAGCTAACCCAG 203
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 204 GCGTCCGCTACTTTCAGAGAGTGACTGTCCATGGGAGTCTGTAAACCATGCTTTTCAC 263
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 264 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATGGACACAGAGAG 323
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 324 TGGGAATTCAAAAGTAGTGGGCAC 347
 RESULT 4
 CO695007 467 bp DNA linear PAT 03-FEB-2004
 LOCUS Sequence 39933 from Patent WO02070737.
 ACCESSION CO695007
 VERSION CO695007.1 GI:42240530
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Liew C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 39933 12-SEP-2002;
 Chondrogene Inc. (CA)
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 /db_xref="taxon:9606"
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
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 Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 80 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 139
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValIleGluCysGlnAlaAsnGln 60
 Db 140 AACTGTGCCATCTCGAGAACCAATTATGGATCTTTGCATAGAAATGTCAGAGCTAACCCAG 199
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 200 GCGTCCGCTACTTTCAGAGAGTGACTGTCCATGGGAGTCTGTAAACCATGCTTTTCAC 259
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 260 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTTGGACACAGAGAG 319
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 320 TGGGAATTCAAAAGTAGTGGGCAC 343
 RESULT 5
 CO712328 471 bp DNA linear PAT 03-FEB-2004
 LOCUS Sequence 57254 from Patent WO02070737.
 ACCESSION CO712328
 VERSION CO712328.1 GI:42273185
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 57254 12-SEP-2002;
 Chondrogene Inc. (CA)
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 Query Match: 100.0% Indels: 0
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 Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 Db 17 ATGGCGGCGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 76
 Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 77 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 136
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValIleGluCysGlnAlaAsnGln 60
 Db 137 AACTGTGCCATCTCGAGAACCAATTATGCATTTGTCATAGAAATGTCAGAGCTAACCCAG 196
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 197 GCGTCCGCTACTTTCAGAGAGTGACTGTCCATGGGAGTCTGTAAACCATGCTTTTCAC 256
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 257 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTTGGACACAGAGAG 316
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 317 TGGGAATTCAAAAGTAGTGGGCAC 340
 RESULT 6
 CO711142 472 bp DNA linear PAT 03-FEB-2004
 LOCUS Sequence 56068 from Patent WO02070737.
 ACCESSION CO711142
 VERSION CO711142.1 GI:42271999
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Liew, C.C., Marshall, W.E. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 56068 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES
source
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Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 41 AsnCysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATGAT 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 GCGTCGCTACTTTCAGAGAGTGTCTGTCGATGGGAGTGTCTGTAACCATGCTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCACATGTCATCTCGCTGGCTCAAAACACGACGAGGTGTCTCCATGGCAACAGAGAG 319
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 320 TGGGAATTCAAAAGTATGGGCAC 343

RESULT 7
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LOCUS BD027641 482 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD027641
VERSION BD027641.1 GI:22569383
KEYWORDS JP 2001269182-A/3887.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 482)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 3887 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/3887
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN

PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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FH Key Location/Qualifiers
FT CDS
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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DB 29 ATGGCGGCGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 88
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 89 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
QY 41 AsnCysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 149 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATGAT 208
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 209 GCGTCGCTACTTTCAGAGAGTGTCTGTCGATGGGAGTGTCTGTAACCATGCTTTTCAC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 269 TTCACATGTCATCTCGCTGGCTCAAAACACGACGAGGTGTCTCCATGGCAACAGAGAG 328
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 329 TGGGAATTCAAAAGTATGGGCAC 352

RESULT 8
AX888031
LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3894 from Patent EP1033401.
ACCESSION AX888031
VERSION AX888031.1 GI:40046785
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 3894 06-SEP-2000;
GENSET

FEATURES
source
1..482
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
29..355
/note="unnamed protein product"
/codon_start=1

/protein_id="CAE93956.1"
/db_xref="GI:40046786"
/translation="MAAAMDVDTPTSGNTSGAGKRFEVKKNAVALWADIIVDNCAL
CRNHMDLCIECOAQASATSEECTVAVGNCNHFPHCI SRMLKTRQVCPLDNREWE
FOKYGH"

ORIGIN

Alignment Scores:
Pred. No.: 2,45e-112 Length: 482
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x AX888031 (1-482)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyValys 20
Db 29 ATGGCGGCGAGTGGATGGATGATACCCCGAGCGGCACCAACAGCGCGGCGCAAGAAG 88
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 89 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
Db 149 AACTGTGCCATCTCGAGAACACCATATGATGATGATGATGATGATGATGATGATGATGATGAT 208
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 209 GCGTCCGCTACTTCAGAAAGATGACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 268
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 269 TTCACATGCACTCTCGCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCT 328
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 329 TGGGAATCCAAAGATATGGGCAC 352

RESULT 9

BD271522 504 bp DNA linear PAT 17-JUL-2003
LOCUS VonHippel-Lindau tumor suppressor complex and novel component of
DEFINITION SCF ubiquitin ligase.
ACCESSION BD271522
VERSION BD271522.1 GI:33081290
KEYWORDS JP 2002541775-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

Conaway,J.W., Conaway,R.C. and Kamura,T.
1 (bases 1 to 504)
VonHippel-Lindau tumor suppressor complex and novel component of
SCF ubiquitin ligase

Patent: JP 2002541775-A 3 10-DEC-2002;
OKLAHOMA MEDICAL RESEARCH FOUNDATION
OS Mus sp. (murine)

PN JP 2002541775-A/3
PD 10-DEC-2002
PF 25-FEB-2000 JP 2000601023

PR 26-FEB-1999 US 60/121787
PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
C12N15/09, A61K38/00, A61K38/53, A61K45/00, A61P35/00, C07K14/47, PC
C12N1/15,

PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P21/02, G01N33/15, G01N33/ PC
50, G01N33/68

CC VonHippel-Lindau tumor suppressor complex and novel component

CC of SCF
FH ubiquitin ligase
FF Key Location/Qualifiers
FT source 1..504
FT /organism="Mus sp. (murine)"

FEATURES

source 1..504
Location/Qualifiers
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

ORIGIN

Alignment Scores:
Pred. No.: 2,55e-112 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD271522 (1-504)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 78 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 137
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
Db 138 AACTGTGCCATCTCGAGAACACCATATGATGATGATGATGATGATGATGATGATGATGATGAT 197
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 198 GCGTCACTACTTCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 258 TTCACATGCACTCTCGATGGCTCAAAACAGCGAGGTGTGCTGCTGGACACAGAGAG 317
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 318 TGGGAGTTCAGAAAGATATGGGCAT 341

RESULT 10

AR640605 504 bp DNA linear PAT 20-APR-2005
LOCUS Sequence 5 from patent US 6858709.
DEFINITION AR640605
ACCESSION AR640605
VERSION AR640605.1 GI:62775414
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 504)
AUTHORS Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE Component of von Hippel-Lindau tumor suppressor complex and SCF
ubiquitin ligase

JOURNAL Patent: US 6858709-A 5 22-FEB-2005;
Oklahoma Medical Research Foundation; Oklahoma City, OK

FEATURES
source 1..504
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2,55e-112 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0


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Qy      21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACGTGTGCCATCTCGAGAAACCAATATGGAATCTTTGCATAGAAATGTCAGACTAACAG 186
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db      187 GCGTCCGCTACTTCAGAGAGTGTCTGCGATGGGAGTGTGTAAACCATGCTTTTCAC 246
Qy      81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      247 TTCCACTGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 306
Qy      101 TrpGluPheGlnLysTyrGlyHis 108
Db      307 TGGGAATTCACAAAGTATGGGCAC 330

RESULT 13
LOCUS   BD271520                      508 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION VonHippel-Lindau tumor suppressor complex and novel component of
            SCF ubiquitin ligase.
ACCESSION BD271520
VERSION   BD271520.1 GI:33081288
KEYWORDS  JP 2002541775-A/1.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 508)
AUTHORS   Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE     VonHippel-Lindau tumor suppressor complex and novel component of
            SCF ubiquitin ligase
JOURNAL   PATENT: JP 2002541775-A 1 10-DEC-2002;
            OKLAHOMA MEDICAL RESEARCH FOUNDATION
COMMENT   OS Homo sapiens (human)
            PN JP 2002541775-A/1
            PD 10-DEC-2002
            PR 26-FEB-1999 US 60/121787
            PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
            C12N15/09,A61K38/00,A61K38/53,A61K45/00,A61P35/00,C07K14/47, PC
            C12N1/15,
            PC C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12P21/02,G01N33/15,G01N33/
            50, G01N33/68
            CC VonHippel-Lindau tumor suppressor complex and novel component
            of SCF
            CC ubiquitin ligase
            CC ubiquitin ligase
            FH Key Location/Qualifiers
            FT source 1..508
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source Location/Qualifiers
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Qy      21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACGTGTGCCATCTCGAGAAACCAATATGGAATCTTTGCATAGAAATGTCAGACTAACAG 186
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db      187 GCGTCCGCTACTTCAGAGAGTGTCTGCGATGGGAGTGTGTAAACCATGCTTTTCAC 246
Qy      81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      247 TTCCACTGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 306
Qy      101 TrpGluPheGlnLysTyrGlyHis 108
Db      307 TGGGAATTCACAAAGTATGGGCAC 330

RESULT 14
LOCUS   AR640603                      508 bp      DNA      linear      PAT 20-APR-2005
DEFINITION Sequence 3 from patent US 6858709.
ACCESSION AR640603
VERSION   AR640603.1 GI:62775412
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 508)
AUTHORS   Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE     Component of von Hippel-Lindau tumor suppressor complex and SCF
            ubiquitin ligase
JOURNAL   Patent: US 6858709-A 3 22-FEB-2005;
            Oklahoma Medical Research Foundation; Oklahoma City, OK
FEATURES  Location/Qualifiers
source 1..508
        /organism="unknown"
        /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,57e-112 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x AR640603 (1-508)
Qy      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db      7  ATGGCGGCGAGCGATGATGTGGATACCCCGAGCGCCACCAACAGCGCGCGGCGCAAGAG 66
Qy      21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACGTGTGCCATCTCGAGAAACCAATATGGAATCTTTGCATAGAAATGTCAGACTAACAG 186
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

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Db 187 GCGTCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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 Db 247 TTCACATGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAG 306
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Qy 101 TrpGluPheGlnLysTyrGlyHis 108
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Db 307 TGGGAATTCCAAAGATGGGCAC 330
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RESULT 15

AF140598 508 bp mRNA linear PRI 11-MAY-1999

LOCUS Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.

DEFINITION AF140598

ACCESSION AF140598

VERSION AF140598.1 GI:4769003

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 508)

AUTHORS Kamura,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J., Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J., Conaway,R.C., Harper,J.W. and Conaway,J.W.

TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase

JOURNAL Science 284 (5414), 657-661 (1999)

PUBMED 10213691

REFERENCE 2 (bases 1 to 508)

AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.

TITLE Direct Submission

JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA

FEATURES

source

1..508

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gene 1..508

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CDS 7..333

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/protein_id="AAD29715.1"

/db_xref="GI:4769004"

/translations="MAAAMDVDTPSGTNSGAGKKRFVKKNAVALWAMDIVVDNCAI CRNHIMDLICIECQANASATSEETVAVGNCNHFHFCISRLWKTRQVCPLDNREWE FQYGH"

ORIGIN

Alignment Scores:

Pred. No.: 2,57e-112 Length: 508

Score: 108.00 Matches: 108

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x AF140598 (1-508)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Db 67 CGCTTTGAAGTGAAGAAAGTGGATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 126
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Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
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Db 127 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 186
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Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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Db 187 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
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Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Db 247 TTCACATGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAG 306
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Qy 101 TrpGluPheGlnLysTyrGlyHis 108
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Db 307 TGGGAATTCCAAAGATGGGCAC 330
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RESULT 16

CQ701366 523 bp DNA linear PAT 03-FEB-2004

LOCUS CQ701366

DEFINITION Sequence 46292 from Patent WO02070737.

ACCESSION CQ701366

VERSION CQ701366.1 GI:42262133

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.

TITLE Compositions and methods relating to osteoarthritis

JOURNAL Patent: WO 02070737-A 46292 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

source

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/organism="Homo sapiens"

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ORIGIN

Alignment Scores:

Pred. No.: 2,64e-112 Length: 523

Score: 108.00 Matches: 108

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x CQ701366 (1-523)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Db 79 CGCTTTGAAGTGAAGAAAGTGGATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 138
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Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
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Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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Db 199 GCGTCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
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Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 |||||

Db 319 TGGGAATTCCAAAGATGGGCAC 342
 |||||

RESULT 17

BC051473
LOCUS
DEFINITION
Mus musculus ring-box 1, mRNA (cdna clone MGC:62905 IMAGE:1430400), complete cds.
ACCESSION
BC051473
VERSION
BC051473.1 GI:30186056
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE

AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 531)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, F.D., Kravitz, S., Kravitz, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (28-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES

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/organism="Mus musculus"
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/strain="C57BL/6J"
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gene

CDS

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ORIGIN

Alignment Scores: 2.69e-112 Length: 531
Pred. No.: 108.00 Matches: 108
Score: 100.00 Conserv: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0% Gaps: 0
DB: 9
US-09-541-462B-2 (1-108) x BC051473 (1-531)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLys 20
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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 73 CGCTTTGAAGTTAAAGAGTGAATGCAATGAGTGGCCCTCTGGGCGCTGGACATTTGGTTGAT 132
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGluAlaAsnGln 60
Db 133 AACTGTGCCATCTCGAGAACCAACATATGGAATCTTTGTATCGAATGTGCAGCCCAACAG 192
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 193 CGCTCAGCTACTTCCGAGAGGTGACGGTTGCATGGGAGGTCTGCAACCATGCTTTTCAT 252
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 253 TTCCACTGCATCTCTCGATGGCTCAAAACGAGCGAGGTGTGTCGCTGGACACAGAGAG 312
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 313 TGGGAGTTCCAGAAAGTATGGGCAT 336

RESULT 18

BC001466
LOCUS
DEFINITION
Homo sapiens ring-box 1, mRNA (cdna clone MGC:1481 IMAGE:3138751), complete cds.
ACCESSION
BC001466
VERSION
BC001466.2 GI:34783098
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Buffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
12477932
2 (bases 1 to 535)

NIH MGC Project
Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:12655214.
Contact: MGC help desk
Email: gcaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
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CONSRSTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSRSTM
TITLE
JOURNAL
REMARK
COMMENT

Alignment Scores:
Pred. No.: 2,69e-112 Length: 535
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

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DEFINITION
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CR456560
ACCESSION
VERSION
CR456560.1 GI:47678650
KEYWORDS
CDNA; chromosome 22; ORF.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS
Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A.,
Cole, C.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y.,
Huckle, E.J., Beare, D.M. and Dunham, I.
TITLE
JOURNAL
PUBMED
15461802
REFERENCE
2 (bases 1 to 535)
AUTHORS
Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A.,
Cole, C.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y.,
Huckle, E.J., Beare, D.M. and Dunham, I.
TITLE
JOURNAL
COMMENT
Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript
Sanger Institute name: pGEM.RBX1
Homo sapiens cDNA sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to isolate cDNA clones
representing the full length open reading frame of well annotated
protein coding genes on human chromosome 22. For more information
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FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 2,696-112 Length: 535
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x CR456560 (1-535)
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LOCUS Homo sapiens ring-box 1, mRNA (cdna clone IMAGE:4065797), partial
DEFINITION cds.
ACCESSION BC017370
VERSION BC017370.1 GI:16924201
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

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TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 554)
 Strausberg, R.
 Direct Submission
 Submitted (13-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
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FEATURES
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gene

CDS

misc_feature

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RESULT 22

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DEFINITION BC027396

ACCESSION BC027396.1 GI:20072075

VERSION MGC.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1616)

AUTHORS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SJ, Wang J, Heich F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Ustin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

CONSRM Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE 12477932

2 (bases 1 to 1616)

DIRECTOR MGC Project.

AUTHORS Direct Submission

TITLE Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 60 Row: 1 Column: 8

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gene

CDS

ORIGIN

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Score: 108.00 Matches: 108

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x BC027396 (1-1616)

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Job time : 2491 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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(without alignments)
1156.486 Million cell updates/sec

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Perfect score: 108
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 12

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
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- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PGTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	482	3	US-09-513-999C-3894
2	108	100.0	504	3	US-09-914-324A-5
3	108	100.0	507	3	US-09-949-016-4940
4	108	100.0	508	3	US-09-914-324A-3
5	84	77.8	3208	3	US-09-780-016-27
6	84	77.8	3208	3	US-10-214-811-27
7	84	77.8	3208	3	US-10-766-074-27
8	74	68.5	411	3	US-09-640-211A-1731
9	55	50.9	402	3	US-09-513-999C-10371

10 55 50.9 463 3 US-09-621-976-15180 Sequence 15180, A
11 40 37.0 301 3 US-09-313-294A-492 Sequence 492, App
12 29 26.9 25274 3 US-09-949-016-16682 Sequence 16682, A
13 12 11.1 480 3 US-09-914-324A-4 Sequence 4, Appli
14 12 11.1 490 3 US-09-270-767-26812 Sequence 26812, A
15 12 11.1 1101 3 US-09-270-767-11265 Sequence 11265, A

ALIGNMENTS

RESULT 1
US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 29..352
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 404
; OTHER INFORMATION: m-a or c
US-09-513-999C-3894

Alignment Scores:
Pred. No.: 1.37e-109 Length: 482
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 29 ATGCGCGACGATGGATGGATACCCGAGCGGCCAACAGCGCGGGCAAGAG 88
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 89 CGCTTTGAAGTGAANAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGGTTGAT 148
Qy 41 AsnCyAlaAlaCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 149 AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTGCATAGAAATGCAAGCTAACCCAG 208
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 209 GCCTCCGCTACTTTCAGAGAGAGTACTGTGCGATGGGAGTCTGTACCAATGCTTTTTCAC 268
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 269 TTCACATGCATCTCTGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 328

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QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 329 TGGGAATTCACAAAGTATGGGCAC 352

RESULT 2
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Alignment Scores:
Pred. No.: 1,42e-109 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 18 ATGGCGCGCGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAAG 77
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 78 CGCTTTGAAGTTAAAGTGAATGCAGTGGCCCTCTGGGCTGGGACATTGGTTGAT 137
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 138 AACTGTGCCATCTCAGCAAGACCAATATGATCTTTGTATCGAATGTCAGGCGCAACAG 197
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 198 CGGTACAGTACTTCCAGAGAGTGTACGGTTGCATGGGAGTCTGCACCATGCTTTTCAT 257
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 258 TTCCACTGCATCTCTCGATGCTCAAAACAGGAGGAGTGTGTCGGTTGGACACAGAGAG 317
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 318 TGGGAGTTCACAAAGTATGGGCAT 341

RESULT 3
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4940
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4940

Alignment Scores:
Pred. No.: 1,43e-109 Length: 507
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 7 ATGGCGCGCGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 67 CGCTTTGAAGTGAAGTGAATGCAGTGGCCCTCTGGGCTGGGATATTGGTTGAT 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 127 AACTGTGCCATCTCAGCAAGACCAATATGATCTTTGGCATAGAAATGTCAGCTAACCCAG 186
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCGTCCGCTACTTCCAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 247 TTCCACTGCATCTCTCGTGGCTCAAAACAGCAGCAGGTGTGTCATTGGACACAGAGAG 306
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 307 TGGGAATTCACAAAGTATGGGCAC 330

RESULT 4
US-09-914-324A-3
; Sequence 3, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25

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; / NUMBER OF SEQ ID NOS: 12
; / SOFTWARE: Patatin Ver. 2.1
; SEQ ID NO 3
; / LENGTH: 508
; / TYPE: DNA
; / ORGANISM: Homo sapiens
; / FEATURE:
; / NAME/KEY: CDS
; / LOCATION: (7)..(333)
; / OTHER INFORMATION: Rbx1
US-914-324A-3

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Alignment Scores:	
Pred. No.:	1.43e-109
Score:	108.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	3
Length:	508
Matches:	108
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-541-462B-2 (1-108) x US-09-914-324A-3 (1-508)

1	MetAlaAlaAlaMetAspValaspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
7	ATGGCGGAGCGAGTGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG	66
21	ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
67	CGCTTTGAAGTGAATAAGTGAATTCGAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	126
41	AsnCysAlaIleCysArgAspHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
127	AACTGTGCATCTCGAGGACCACATTATGGATCTTTGCATAGAACTCAAGCTAACCCAG	186
61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
187	GGTCCGCTACTTCAGAAAGAGTGTACTGTCCATGGGGAGTCTGTAAACATGCTTTTCAC	246
81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
247	TTCCACTGCATCTCTCGTGGCTCAAAACACGACAGAGTGTGTCCATTGGACAACACAGAGAG	306
101	TrpGluPheGlnLysTyrGlyHis	108
307	TGGGAATTCCAAAAGATATGGGCAC	330

RESULT 5
US-09-780-016-27

```

; APPLICANT: Sands, Arthur I.
; TITLE OF INVENTION: No. 6509456el Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208

```

;;
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-09-780-016-27

Alignment Scores:	1.71e-82	Length:	3208
Pred. No.:	84.00	Matches:	84
Score:	Percent Similarity:	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	77.8%	Indels:	0
DB:	3	Gaps:	0

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

	QY	25	LysLysTrpAsnAlavalalaleuTrpAlatrpAspilevalvalasphenCysallaile	44
	DB	2770	AAAAATGGAATGCAGTAGCCCTCGGGCTGGATATTGTGGTTGATAACTGTGCCATC	2829
	QY	45	CysArgAsnHisfileMetAspLeuCysyleGluCysGlnAlaAsnGlnlaserAlatr	64
	DB	2830	TGCAGGAACCAATTATGGATCTTTGCATAGAATGTCAAGCTAACACAGGGCTCCGTACT	2889
	QY	65	SerGluGluCysThrvalalalaTrpGlyValCysAsnHisAlaphHisPheHiscysille	84
	DB	2890	TACAAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCACCTCCACTGCATC	2949
	QY	85	SerArgTrpLeuLysThrsArgGlnValCysProLeuAspAsnArgGlnurpGluPheGln	104
	DB	2950	TCTCGCTGGCTCAAACACGACAGAGTGTTGTCATTGGACACAGAGAGTGGGAATCCAA	3009
	QY	105	LysTyrGlyHis	108
	DB	3010	AAGTATGGGCAC	3021

```

RESULT 6
US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6743621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743621el Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

```

Alignment Scores:	1.71e-82	Length:	3208
Pred. No.:	84.00	Matches:	84
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	77.8%	Gaps:	0
DB:	3		

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
2770 AAAAAATGGAATGCAGTAGCCCTCGGGCTGGGATATTGTGGTTGATAACTGTGGCATC
Db

QY 45 CysArgAsnHisIleMetAspLeuValCysGlnAlaValAspAsnGlnAlaSerAlaThr 64
 DB 2830 TGCAGGAACACATTATGGATCTTTGTCATAGATGTAACAGCTAACAGGGCGTCCGCTACT 2889
 QY 65 SerGluGluCysThrValAlaLalaValCysAsnHisAlaPheHisPheHisCysIle 84
 DB 2890 TCAGAGAGTGTACTGTGGCATGGGAGTGTGTACCACTGCTTTTCACTTCCACTGCATC 2949
 QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
 DB 2950 TCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAATTCCAA 3009
 QY 105 LysTyrGlyHis 108
 DB 3010 AAGTATGGGCAC 3021

RESULT 7
 US-10-766-074-27
 ; Sequence 27, Application US/10766074
 ; Patent No. 6881563
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6881563el Human Proteases and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10766,074
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR FILING DATE: 2002-08-07
 ; PRIOR FILING DATE: 2002-08-07
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 3208
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-766-074-27

Alignment Scores:
 Pred. No.: 1.71e-82 Length: 3208
 Score: 84.00 Matches: 84
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 77.8% Indels: 0
 DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-766-074-27 (1-3208)
 QY 25 LysLysTrpAsnAlaValAlaLalaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
 DB 2770 AAAAATGGAATGATGATAGCCCTTGGCGCTGGATATTGGTTGATTAATGTCCTACT 2829
 QY 45 CysArgAsnHisIleMetAspLeuValCysGlnAlaValAspAsnGlnAlaSerAlaThr 64
 DB 2830 TGCAGGAACACATTATGGATCTTTGTCATAGATGTAACAGCTAACAGGCGTCCGCTACT 2889
 QY 65 SerGluGluCysThrValAlaLalaValCysAsnHisAlaPheHisPheHisCysIle 84
 DB 2890 TCAGAGAGTGTACTGTGGCATGGGAGTGTGTACCACTGCTTTTCACTTCCACTGCATC 2949
 QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
 DB 2950 TCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAATTCCAA 3009

QY 105 LysTyrGlyHis 108
 DB 3010 AAGTATGGGCAC 3021
 RESULT 8
 US-09-640-211A-1731
 ; Sequence 1731, Application US/09640211A
 ; Patent No. 6833446
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Marion
 ; APPLICANT: Shenk, Michael A.
 ; APPLICANT: McGrath, Annette
 ; APPLICANT: Glenn, Matthew
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; FILE REFERENCE: Modification of Gene Transcription
 ; FILE REFERENCE: 11000.1021C1U
 ; CURRENT APPLICATION NUMBER: US/09/640,211A
 ; CURRENT FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 2368
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1731
 ; LENGTH: 411
 ; TYPE: DNA
 ; ORGANISM: Pinus radiata
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(411)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-640-211A-1731
 Alignment Scores:
 Pred. No.: 2.49e-72 Length: 411
 Score: 74.00 Matches: 74
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 68.5% Indels: 0
 DB: 3 Gaps: 0
 US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)
 QY 25 LysLysTrpAsnAlaValAlaLalaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
 DB 176 AAGAAGTGAATGCTGTAGCCCTTGGCGCTGGATATTGGTTGATTAATTTGCAATT 235
 QY 45 CysArgAsnHisIleMetAspLeuValCysGlnAlaValAspAsnGlnAlaSerAlaThr 64
 DB 236 TGCAGGAACACACATCATGGACCTCTGTATTGAGTGTCTCAGGCAATCAAGCAAGTGCACCA 295
 QY 65 SerGluGluCysThrValAlaLalaValCysAsnHisAlaPheHisPheHisCysIle 84
 DB 296 AGTGAAGAATGATGTTGTCATGGGTTGTTGCAATCAGCCCTTCAATTCATTGCGATA 355
 QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98
 DB 356 AGTCGGTGGCTCAAGACACGACAGTCTGCCCATTTAGATAAT 397
 RESULT 9
 US-09-513-999C-10371
 ; Sequence 10371, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm


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; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

Alignment Scores:
Pred. No.: 2,66e-21 Length: 25274
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.9% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-16682 (1-25274)

Qy 77 HisAlaPheHisPheHisCysIleSerArgTrrPleuLysThrArgGlnValCysProLeu 96
Db 18411 CATGCTTTTTCACITTCCTCACTGCACTCTCGCTGGCTCAAAACACGACGAGGTGTCCATTG 18470

Qy 97 AspAsnArgGluTrpGluPheGlnLys 105
Db 18471 GACACAGACAGTGGGAATTCCTCAAAAG 18497

RESULT 13
US-09-914-324A-4
; Sequence 4, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rbx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 0.00033 Length: 480
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-4 (1-480)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 157 GTTGACAACTGTGTATTGTCAGGAACCATATAATG 192

RESULT 14
US-09-270-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11265
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11265

Alignment Scores:
Pred. No.: 0.000704 Length: 1101
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-11265 (1-1101)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 867 GTTGACAACTGTGTCCATCTGCCGTAAACCATCATG 832

Search completed: March 11, 2006, 09:40:59
Job time : 171 secs

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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26812
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26812

Alignment Scores:
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Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-26812 (1-490)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 256 GTTGACAACTGTGTCCATCTGCCGTAAACCATCATG 221

RESULT 15
US-09-270-767-11265/c
; Sequence 11265, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11265
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11265

Alignment Scores:
Pred. No.: 0.000704 Length: 1101
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-11265 (1-1101)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 867 GTTGACAACTGTGTCCATCTGCCGTAAACCATCATG 832

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 09:45:04 ; Search time 653 Seconds
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Title: US-09-541-462B-2

Perfect score: 108

Sequence: 1 MAAAMDVTPGTSGAGK.....KTRQVCLDNREWFQYKH 108

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Searched: 9793542 seqs, 4134689005 residues

Word size: 12

Total number of hits satisfying chosen parameters: 119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=12
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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	108	100.0	433	7	US-10-085-783A-43377
3	108	100.0	453	7	US-10-242-535A-35025
4	108	100.0	453	7	US-10-085-783A-35025
5	108	100.0	467	7	US-10-242-535A-39933
6	108	100.0	467	7	US-10-085-783A-39933
7	108	100.0	471	7	US-10-242-535A-57254

8	108	100.0	471	7	US-10-085-783A-57254	Sequence 57254, A
9	108	100.0	472	7	US-10-242-535A-56068	Sequence 56068, A
10	108	100.0	472	7	US-10-085-783A-56068	Sequence 56068, A
11	108	100.0	504	8	US-10-913-937-5	Sequence 5, Appli
12	108	100.0	508	8	US-10-913-937-3	Sequence 3, Appli
13	108	100.0	523	7	US-10-242-535A-46292	Sequence 46292, A
14	108	100.0	523	7	US-10-085-783A-46292	Sequence 46292, A
15	107	99.1	476	3	US-09-918-995-17191	Sequence 17191, A
16	106	98.1	4543	5	US-10-198-846-11311	Sequence 11311, A
17	103	95.4	4476	8	US-10-357-930-25604	Sequence 25604, A
18	98	90.7	3484	8	US-10-723-860-1383	Sequence 1383, Ap
19	98	90.7	3484	9	US-10-756-149-1357	Sequence 1357, Ap
20	98	90.7	5111	5	US-10-205-823-382	Sequence 382, App
21	98	90.7	5111	10	US-11-051-454-382	Sequence 382, App
22	98	90.7	5371	8	US-10-723-860-5852	Sequence 5852, Ap
23	95	88.0	430	7	US-10-242-535A-54751	Sequence 54751, A
24	95	88.0	430	7	US-10-085-783A-54751	Sequence 54751, A
25	90	83.3	468	7	US-10-242-535A-47656	Sequence 47656, A
26	90	83.3	468	7	US-10-085-783A-47656	Sequence 47656, A
27	90	83.3	5347	6	US-10-240-965-39	Sequence 99, Appl
28	87	80.6	380	3	US-09-960-352-4677	Sequence 4677, Ap
29	84	77.8	3208	3	US-09-780-016-27	Sequence 27, Appl
30	84	77.8	3208	5	US-10-214-811-27	Sequence 27, Appl
31	84	77.8	3208	7	US-10-766-074-27	Sequence 27, Appl
32	84	77.8	3208	10	US-11-036-185-27	Sequence 27, Appl
33	83	76.9	692	10	US-11-097-143-31031	Sequence 31031, A
34	74	68.5	411	8	US-10-856-499-1731	Sequence 1731, Ap
35	74	68.5	527	9	US-10-487-901-4266	Sequence 4266, Ap
36	74	68.5	531	9	US-10-487-901-4271	Sequence 4271, Ap
37	74	68.5	617	9	US-10-487-901-4265	Sequence 4265, Ap
38	74	68.5	619	7	US-10-425-114-25647	Sequence 25647, A
39	74	68.5	673	9	US-10-487-901-4262	Sequence 4262, Ap
40	74	68.5	731	9	US-10-487-901-4264	Sequence 4264, Ap
41	74	68.5	840	7	US-10-767-701-12172	Sequence 12172, A
42	70	64.8	390	3	US-09-770-791-20	Sequence 20, Appl
43	70	64.8	553	7	US-10-021-323-10545	Sequence 10545, A
44	70	64.8	608	8	US-10-767-795-687	Sequence 687, App
45	70	64.8	831	8	US-10-767-795-2752	Sequence 2752, Ap

ALIGNMENTS

RESULT 1

US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377

Alignment Scores:
Pred. No.: 9,41e-111 Length: 433
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

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QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 20 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATGGTTGAT 139
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTGCAGGACCAACATATATGATCTTTGCATAGAAATGCTAAGCTAACCCAG 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTCTCCATTGGCAACAGAGAG 319
QY 101 TrpGluPheGlnLysTyrglyHis 108
DB 320 TGGGAATTCAAAAGATGGGCAC 343

RESULT 2

US-10-085-783A-43377
Sequence 43377, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patent in version 3.2
SEQ ID NO 43377
LENGTH: 433
TYPE: DNA
ORGANISM: Human

Alignment Scores:
Pred. No.: 9,41e-111 Length: 433
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 20 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATGGTTGAT 139

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTGCAGGACCAACATATATGATCTTTGCATAGAAATGCTAAGCTAACCCAG 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTCTCCATTGGCAACAGAGAG 319
QY 101 TrpGluPheGlnLysTyrglyHis 108
DB 320 TGGGAATTCAAAAGATGGGCAC 343

RESULT 3

US-10-242-535A-35025
Sequence 35025, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patent in version 3.2
SEQ ID NO 35025
LENGTH: 453
TYPE: DNA
ORGANISM: Human

Alignment Scores:
Pred. No.: 9,79e-111 Length: 453
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-35025 (1-453)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 24 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 83
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 84 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATGGTTGAT 143
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 144 AACTGTGCCATCTGCAGGACCAACATATATGATCTTTGCATAGAAATGCTAAGCTAACCCAG 203
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 204 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTTCAC 263
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTCTCCATTGGCAACAGAGAG 323

Db	197	GGGTCCGGCTACTTTCAGAGAGTGTTACTGTCCGATGGGGAGTGTGTAACCATGCTTTTCAC	256
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	257	TTCACATGCATCTCTCGTGGCTCAAAACACACAGAGGTGTGTCCATTGGACACACAGAG	316
Qy	101	TrpGluPheGlnLysTyrGlyHis	108
Db	317	TGGGAATTCAAAAGTATGGGCAC	340

RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 56068
; LENGTH: 472

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QY	21	ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	80	CGCTTTGAAGTGAAAAAGTGGAAATGCGAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT	139
QY	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	140	AACGTGCCATCTCGAGGAACCAATATGCGATCTTTGCATGAATGTCAAGCTAACCAAG	199
QY	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	200	GGCTCCGCTACTCTCAGAAAGAGTGACTGTGCGATGGGGAGTCTGTAAACCATCTCTTTTTCAC	259
QY	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100

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Db      260  TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACACAGAGAG 319
Qy      101  TipGluPheGlnLysTyrGlyHis 108
Db      320  TGGGAATTCCAAAAGTATGGGCAC 343

RESULT 10
US-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-56068

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Qy	1	MetAlaAlaMetAspValaspThrProSerGlyThrAsnSerGlyValaGlyLysLys	20
Db	20	ATGGCGCAGCGATGGATGTGGATATCCCGAGCGGCACCAACAGCGCGCGGGCAAGAAG	79
Qy	21	ArgPheGluValLysLysThrAsnAlaValAlaLeuTrpAlaTrpAspIleValValasp	40
Db	80	CGCTTTCAAGTGAATAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTGTGAT	139
Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	140	AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTTGCATAGAGAAATGTCAGAGCTAAACCAG	199
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	200	GGCTCGCTACTTTCAGAAAGAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTTCAC	259
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	260	TTCCACTGCTATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCTCCATTGGACAACAGAGAG	319
Qy	101	TrpGluPheGlnLysTyrGlyHis	108
Db	320	TGGGAATTCAAAAGATATGGGCAC	343

RESULT 11
 US-10-913-937-5
 ; Sequence 5, Application US/10913937
 ; Publication No. US20050019813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Joan A.
 ; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Kamura, Takumi
 ; APPLICANT: Oklahoma Medical Research Foundation
 ; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
 ; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
 ; FILE REFERENCE: 021044-004600US
 ; CURRENT APPLICATION NUMBER: US/10/913,937
 ; CURRENT FILING DATE: 2004-08-05
 ; PRIOR APPLICATION NUMBER: US/09/914,324
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: US 60/121,787
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 504
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (18)..(344)
 ; OTHER INFORMATION: Rbx1
 US-10-913-937-5

Alignment Scores:
 Pred. No.: 1,08e-110 Length: 504
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-5 (1-504)

Qy	1	MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
Db	18	ATGGCGCGCGATGGATGTGGATACCCCGCGGCGCCCAACAGCGCGCGGCAAG	77
Qy	21	ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	78	CGCTTTGAAGTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGACATTTGGTTGAT	137
Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	138	AACGTGCCATCTCCAGAACCACTATATGGATCTTTGTATCGAATGTCAGGCCAACAG	197
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	198	CGGTGAGTACTTCCGAAGAGTGTACGTTGCATGGGAGTCTGCAACCATGCTTTTCAT	257
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	258	TTCCACTGCATCTCTCGATGCTCAAAACGAGGAGGTGTGTCGTTGGACAAACAGAG	317
Qy	101	TrpGluPheGlnLysTrpGlyHis	108
Db	318	TGGGAGTTCCAAAGTATGGGCAT	341

RESULT 12
 US-10-913-937-3
 ; Sequence 3, Application US/10913937
 ; Publication No. US20050019813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Joan A.

; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Kamura, Takumi
 ; APPLICANT: Oklahoma Medical Research Foundation
 ; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
 ; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
 ; FILE REFERENCE: 021044-004600US
 ; CURRENT APPLICATION NUMBER: US/10/913,937
 ; CURRENT FILING DATE: 2004-08-05
 ; PRIOR APPLICATION NUMBER: US/09/914,324
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: US 60/121,787
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 508
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(333)
 ; OTHER INFORMATION: Rbx1
 US-10-913-937-3

Alignment Scores:
 Pred. No.: 1,08e-110 Length: 508
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-3 (1-508)

Qy	1	MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
Db	7	ATGGCGCGCGATGGATGTGGATACCCCGCGGCGCCCAACAGCGCGCGGCAAG	66
Qy	21	ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	67	CGCTTTGAAGTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGATATTGGTTGAT	126
Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
Db	127	AACGTGCCATCTCCAGAACCACTATATGGATCTTTGTATCGAATGTCAGGCCAACAG	186
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	187	CGGTGAGTACTTCCGAAGAGTGTACGTTGCATGGGAGTCTGTAACCATGCTTTTCAC	246
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	247	TTCCACTGCATCTCTCGATGCTCAAAACGAGGAGGTGTGTCGTTGGACAAACAGAG	306
Qy	101	TrpGluPheGlnLysTrpGlyHis	108
Db	307	TGGGAGTTCCAAAGTATGGGCAC	330

RESULT 13
 US-10-242-535A-46292
 ; Sequence 46292, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liaw, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28

;; PRIOR APPLICATION NUMBER: US 60/305,340
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/275,017
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: US 60/271,955
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 58994
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 46292
;; LENGTH: 523
;; TYPE: DNA
;; ORGANISM: Human
US-10-085-783A-46292

Alignment Scores:
Pred. No.: 1.11e-110 Length: 523
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 19 ATGGCGGCGAGTGGATGTGGATACCCGAGCGGCACCAACAGCGCGGCAAGAAG 78
Qy 21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 79 CGCTTTGAAGTGAAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 139 AACTGTGCCATCTCAGAAAGAGTGTCTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
Qy 81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 259 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 318
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 319 TGGGAATTCAAAAGATATGGGCAC 342

RESULT 14

US-10-085-783A-46292
; Sequence 46292, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-46292

Alignment Scores:
Pred. No.: 1.11e-110 Length: 523
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 19 ATGGCGGCGAGTGGATGTGGATACCCGAGCGGCACCAACAGCGCGGCAAGAAG 78
Qy 21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 79 CGCTTTGAAGTGAAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 139 AACTGTGCCATCTCAGAAAGAGTGTCTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 198
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 199 GCGTCCGCTACTTCCAGAAAGAGTGTCTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
Qy 81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 259 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 318
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 319 TGGGAATTCAAAAGATATGGGCAC 342

RESULT 15

US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-17191

Alignment Scores:

Pred. No.: 1.34e-109 Length: 476
Score: 107.00 Matches: 107
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

Qy 2 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 75 GCGGCGAGTGGATGTGGATACCCGAGCGGCACCAACAGCGCGGCAAGAAGCGC 134

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:30:45 ; Search time 494 Seconds
(without alignments)
1457.058 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 108

Sequence: 1 MAAAMDVDTSGTNSGAGK.....KTRQVCPDNRWSEFKYGH 108

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 12

Total number of hits satisfying chosen parameters: 95

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=12 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absc03h
-USRR=US09541462 @CGN 1 1 727 @runat_10032006_080830_22345 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -BSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -YGAPOP=6 -YGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	100.0	327	3 AAA96882	Aaa96882 Nucleotide
2	108	100.0	482	3 AAC03896	Aac03896 Human sec
3	108	100.0	504	3 AAA74980	Aaa74980 DNA encod
4	108	100.0	506	12 ADQ87496	Adq87496 Human tum

5	108	100.0	506	12	ADQ87156	Adq87156 Human tum
6	108	100.0	506	13	ADQ84881	Adq84881 Human tum
7	108	100.0	508	3	AAA74978	Aaa74978 DNA encod
8	108	100.0	508	13	ACN40951	Acn40951 Tumour-as
9	107	99.1	476	9	ACH29979	Ach29979 Human tes
c 10	106	98.1	3726	13	ADS09913	Adso9913 Human the
c 11	106	98.1	4543	11	ACN90161	Acn90161 Breast ca
c 12	105	97.2	503	12	ADQ92179	Adq92179 Human aut
13	105	97.2	539	5	AAH97860	Aah97860 Murine 7-
14	105	97.2	586	5	AAH97862	Aah97862 Murine 7-
c 15	103	95.4	4476	5	ABV25615	Abv25615 Human pro
c 16	98	90.7	311	14	ACL57420	ACL57420 Human col
c 17	98	90.7	3484	12	ADF42703	Adf42703 Human tes
c 18	98	90.7	3484	12	ADQ18564	Adq18564 Human sof
c 19	98	90.7	3484	13	ADQ80865	Adq80865 Human SPA
c 20	98	90.7	5111	10	ADB75558	Adb75558 Prostate
c 21	98	90.7	5371	12	ADQ23032	Adq23032 Human sof
c 22	90	83.3	485	3	AAA43288	Aaa43288 Xenopus s
c 23	87	80.6	3347	6	AAS94844	Aas94844 Human DNA
c 24	87	80.6	380	8	ABX39512	Abx39512 Bovine ES
25	84	77.8	3208	4	AAD12859	Aad12859 Human nov
26	83	76.9	692	4	ABL22527	Abi22527 Drosophil
27	74	68.5	411	3	AAC57009	Aac57009 Pinus rad
28	74	68.5	527	10	ADK56883	Adk56883 Plant DNA
29	74	68.5	531	10	ADK56888	Adk56888 Plant DNA
30	74	68.5	617	10	ADK56882	Adk56882 Plant DNA
31	74	68.5	619	13	ADX50907	Adx50907 Plant ful
32	74	68.5	673	10	ADK56879	Adk56879 Plant DNA
33	74	68.5	721	14	AEB66106	Aeb66106 Rice geno
34	74	68.5	731	10	ADK56881	Adk56881 Plant DNA
c 35	72	66.7	502	14	ADY78665	Ady78665 Human CDN
36	70	64.8	390	6	ABQ85150	Abq85150 Arabidops
c 37	70	64.8	553	13	ACN55764	Acn55764 Cotton an
38	70	64.8	608	13	ADR59906	Adr59906 Cotton CD
39	70	64.8	635	3	AAC39854	Aac39854 Arabidops
40	70	64.8	831	13	ADR61971	Adr61971 Cotton CD
41	69	63.9	509	5	AAS68845	Aas68845 DNA encod
42	67	62.0	586	10	ADK56887	Adk56887 Plant DNA
43	67	62.0	691	10	ADK56880	Adk56880 Plant DNA
44	66	61.1	2841	4	ABL22526	Abi22526 Drosophil
45	58	53.7	342	12	ADG99381	Adg99381 Kidney di

ALIGNMENTS

RESULT 1
AAA96882
ID AAA96882 standard; DNA; 327 BP.

XX
AC AAA96882;

DT 19-FEB-2001 (first entry)

XX Nucleotide sequence of human ring finger protein ROC1.

DE ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
tumour; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..327

FT /*tag= a

FT /product= "ROC1"

XX WO200058472-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008592.

XX PR 31-MAR-1999; 99US-0127261P.


```

Db      329 TGGGAATTCCTCAAAAGTATGGGCAC 352
RESULT 3
AAA74980
ID      AAA74980 standard; DNA; 504 BP.
XX
AC      AAA74980;
XX
DT      02-JAN-2001 (first entry)
XX
DE      DNA encoding a murine cullin-interacting RING-H2 finger protein (Rbx1).
XX
KW      Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
KW      tumour suppressor; carcinoma; Ring box associated carcinoma;
KW      von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
KW      cerebellar hemangioblastoma; hemangioma; retinal angioma;
KW      pheochromocytoma; ss.
XX
OS      Mus sp.
XX
FN      WO200050445-A1.
XX
PD      31-AUG-2000.
XX
PF      25-FEB-2000; 2000WO-US004838.
XX
PR      26-FEB-1999; 99US-0121787P.
XX
PA      (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI      Conaway JA, Conaway RC, Kamura T;
XX
DR      WPI; 2000-572067/53.
XX
PT      Cullin interacting RING-H2 finger protein, a component of von Hippel-
PT      Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
PT      ubiquitin ligase, useful for diagnosing and treating Ring box protein
PT      associated carcinomas.
XX
PS      Disclosure; Page 35; 37pp; English.
XX
CC      The present sequence encodes a murine cullin-interacting RING-H2 finger
CC      protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
CC      is a tumour suppressor. Human Rbx1 is useful for diagnosing a
CC      predisposition of a patient to certain carcinomas. It is also useful for
CC      treating Ring box protein associated carcinomas or augmenting
CC      metabolically deficient system in animals. Human Rbx1 is also useful for
CC      evaluating the effectiveness of a therapeutic treatment for Ring box
CC      associated carcinomas. Human Rbx1 can be used to screen for agents which
CC      augment or inhibit the activity of other cullin-containing ubiquitin
CC      ligase and of the VHL (von Hippel-Lindau) complex controlling the
CC      conjugation of ubiquitin or ubiquitin-like proteins to various sets of
CC      target proteins. Carcinomas which may be treated include renal
CC      carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal
CC      angioma and pheochromocytomas
XX
SQ      Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.:      2,72e-106      Length:      504
Score:          108.00      Matches:      108
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:              3      Gaps:         0
US-09-541-462b-2 (1-108) x AAA74980 (1-504)
Qy      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLeuLys 20
Db      18 ATGCGCGCGCGATGGTGTGGATACCCCGAGCGCCACCAACGCGCGGCAAGAG 77
Qy      21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      78 CGCTTTGAAGTTAAAAAGTGAATGCAATGCGAGTGGCCCTCTGGGCTGGGACATTGTGTTGAT 137
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGluAlaAsnGln 60
Db      138 AACTGTGCCATCTCGAGAACCACTATATGATCTTTGTATCGAATGTCAGGCCAACACAG 197
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaAlaTrpGlyValCysAsnHisAlaPheHis 80
Db      198 GCGTCAGCTACTTCCGAAGAGTGTACGGTTCATGGGAGTCTGCAACCATGCTTTTCAT 257
Qy      81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      258 TTCCATGCTCATCTCTCGATGCTCAAAACGAGGAGGTGTGTCGTTGGACACAGAGAG 317
Qy      101 TrpGluPheGlnLysTyrGlyHis 108
Db      318 TGGGAGTTCAGAAAGTATGGGCAT 341
RESULT 4
ADQ87496
ID      ADQ87496 standard; cDNA; 506 BP.
XX
AC      ADQ87496;
XX
DT      07-OCT-2004 (first entry)
XX
DE      Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
XX
KW      human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW      cancer; cell proliferative disorder; gene; ss.
XX
OS      Homo sapiens.
XX
FN      WO2004060270-A2.
XX
PD      22-JUL-2004.
XX
PF      15-OCT-2003; 2003WO-US029126.
XX
PR      18-OCT-2002; 2002US-0418988P.
XX
PA      (GETH ) GENENTECH INC.
PA      (WUTD/) WU T D.
PA      (ZHOU/) ZHOU Y.
XX
PI      Wu TD, Zhou Y;
XX
DR      WPI; 2004-534300/51.
XX
PT      New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT      preventing or treating cell proliferative disorders such as cancer.
XX
PS      Claim 1; SEQ ID NO 4374; 5504pp; English.
XX
CC      The present invention describes an isolated tumour-associated antigenic
CC      target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC      sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC      (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC      sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC      (c). Also described: (1) an expression vector comprising the above
CC      nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC      a process for producing a polypeptide; (4) an isolated polypeptide
CC      comprising: (a) an amino acid sequence encoded by any of the above
CC      nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC      length coding region of the above nucleotide sequences; or (c) a sequence
CC      having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC      comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC      an isolated antibody that binds to the above polypeptide; (7) a process
CC      for producing the antibody; (8) an isolated oligopeptide that binds to
CC      the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC      binding organic molecule that binds to the above polypeptide; (10) a

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CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ87496 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 6 ATGGCGGCGAGTGGATGGATGGATACCCGAGCGGCGACCAACGCGCGCGGCAAGAG 65
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 66 CGCTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 126 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCATAGAAATCTCAAGCTAACCCAG 185
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 186 GCGTCCGCTACTTCAGAAAGAGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 245
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 246 TTCACATGTCATCTCGCTGGCTCAAAACAGCAGAGTGTGTCTCATTTGGACACAGAGAG 305
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 306 TGGGAATTCAAAAGTATGGGCAC 329

RESULT 5
ADQ87156
ID ADQ87156 standard; cDNA; 506 BP.
XX
AC ADQ87156;

XX 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
DE human; tumour-associated antigenic target; TAR; cytostatic; gene therapy;
XX human; tumour-associated antigenic target; TAR; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX

PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
XX WPI; 2004-534300/51.
DR
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 4032; 5504pp; English.
XX

CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ87156 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db 6 ATGGCGGAGGATGGATGGATATCCCGAGCGGCAACACAGCGCGGCGGAAGAAG 65
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 66 CGCTTTGAAGTGAAAGAGTGAATGCAGTACCTCTGGGCTGGGATATTGGTTGAT 125
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 126 AACTGTGCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 185
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 186 GCGTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTGTGAACCATGCTTTTCAC 245
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 246 TTCCACTCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 305
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 306 TGGGAATTCCTCAAAAGTATGGGCAC 329

RESULT 6

ADQ84881

ID ADQ84881 standard; cDNA; 506 BP.

XX AC ADQ84881;

XX DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #1695.

XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

XX KW cancer; cell proliferative disorder; gene; ss.

XX OS Homo sapiens.

XX PN WO2004060270-A2.

XX PD 22-JUL-2004.

XX PF 15-OCT-2003; 2003WO-US029126.

XX PR 18-OCT-2002; 2002US-0418988P.

XX PA (GETH) GENENTECH INC.

XX PA (WUTD/) WU T D.

XX PA (ZHOU/) ZHOU Y.

XX PI Wu TD, Zhou Y;

XX PI WPI; 2004-534300/51.

XX PT New nucleic acid molecule and encoded polypeptide, for diagnosing,

XX PT preventing or treating cell proliferative disorders such as cancer.

XX PS Claim 1; SEQ ID NO 1695; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ84881 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db 6 ATGGCGGAGGATGGATGGATATCCCGAGCGGCAACACAGCGCGGCGGAAGAAG 65

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40

Db 66 CGCTTTGAAGTGAAAGAGTGAATGCAGTACCTCTGGGCTGGGATATTGGTTGAT 125

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

Db 126 AACTGTGCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 185

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Db 186 GCGTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTGTGAACCATGCTTTTCAC 245

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 246 TTCCACTCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 305

Qy 101 TrpGluPheGlnLysTyrGlyHis 108

Db 306 TGGGAATTCCTCAAAAGTATGGGCAC 329

RESULT 7

AAA74978

ID AAA74978 standard; DNA; 508 BP.

XX AC AAA74978;

XX DT 02-JAN-2001 (first entry)

XX DE DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).

XX KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;

XX KW tumour suppressor; carcinoma; Ring box associated carcinoma;

KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 KW cerebellar hemangioblastoma; hemangioma; retinal angioma;
 XX pheochromocytomas; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..333
 FT /*tag= a
 FT /product= "cullin-interacting RING-H2 finger protein
 FT (Rbx1)"
 XX
 PN WO200050445-A1.
 XX
 XX 31-AUG-2000.
 XX
 XX 25-FEB-2000; 2000WO-US004838.
 XX
 XX 26-FEB-1999; 99US-0121787P.
 XX
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 XX Conway JA, Conway RC, Kamura T;
 XX
 XX WPI; 2000-572067/53.
 DR P-PSDB; AAB08813.
 XX
 XX Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.
 XX
 XX Claim 3; Page 35; 37pp; English.
 XX
 XX The present sequence encodes a human cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The polypeptide is a tumour
 CC suppressor. Rbx1 is useful for diagnosing a predisposition of a patient
 CC to certain carcinomas. It is also useful for treating Ring box protein
 CC associated carcinomas or augmenting metabolically deficient system in
 CC animals. Rbx1 is also useful for evaluating the effectiveness of a
 CC therapeutic treatment for Ring box associated carcinomas. Rbx1 can be
 CC used to screen for agents which augment or inhibit the activity of other
 CC cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau)
 CC complex controlling the conjugation of ubiquitin or ubiquitin-like
 CC proteins to various sets of target proteins. Carcinomas which may be
 CC treated include renal carcinomas, cerebellar hemangioblastomas and
 CC hemangiomas, retinal angioma and pheochromocytomas
 XX
 XX Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2,74e-106 Length: 508
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-09-541-462B-2 (1-108) x AAA74978 (1-508)
 QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 7 ATGGCGGAGGATGGATGGATACCCGCGGCGCACCAACAGCGCGGCGGAAGAAG 66
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 67 CGCTTTGAAGTGAAAGAGTGAATGACAGTACGCTCTGGGCTGGGATTTGTGTTGAT 126
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 DB 127 AACTGTGCATCTGCAGGAGACACATATTGATCTTTGCATAGATGTCAAGCTAACCCAG 186
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

DB 187 GCGTCGCTACTTCAGAGGTGACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
 QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 247 TTCCTACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 306
 QY 101 TrpGluPheGlnLysTyrGlyHis 108
 DB 307 TGGGAATTCCAAAGATATGGGCAC 330
 RESULT 8
 ACN40951
 ID ACN40951 standard; cDNA; 508 BP.
 XX
 XX ACN40951;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Tumour-associated antigenic target (TAT) cDNA DNA326980, SEQ ID NO:6072.
 XX
 XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004030615-A2.
 XX
 XX 15-APR-2004.
 XX
 XX 29-SEP-2003; 2003WO-US028547.
 XX
 XX 02-OCT-2002; 2002US-0414971P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Wu TD, Zhang Z, Zhou Y;
 XX
 XX WPI; 2004-347921/32.
 DR P-PSDB; ABM82365.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 1; SEQ ID NO 6072; 7273pp; English.
 XX
 XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention

XX SQ Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2.74e-106 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
US-09-541-462B-2 (1-108) x ACN40951 (1-508)
Qy 1 MetalAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAG 66
Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 67 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 126
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTGCAGAACCAACATATGATCTTTCATAGATGTCAAGCTAACAG 186
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTCAGAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAG 306
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 307 TGGGAATCCAAAAGTATGGGCAC 330
RESULT 9
ACH29979
ID ACH29979 standard; cDNA; 476 BP.
XX AC ACH29979;
XX 13-OCT-2003 (first entry)
XX Human testis cDNA #365.
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
XX US2003073623-A1.
XX 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating

antisense DNA or RNA.
Claim 1; SEQ ID NO 17191; 44pp; English.
The invention relates to an isolated polynucleotide comprising any one of
38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was
determined by the technique of SBH (sequencing by hybridisation). Also
included is a purified polypeptide comprising a sequence corresponding to
a reading frame of the novel polynucleotide. The nucleic acid sequences
are useful in diagnostics as expressed sequence tags (EST) for
identifying expressed genes or for physical mapping of the human genome,
in forensics, in assessing biodiversities, or in identifying mutations
responsible for genetic disorders and other traits. The nucleotide
sequences are also useful as hybridisation probes, as oligomers for PCR,
for chromosome and gene mapping, in the recombinant production of
protein, or in generating antibodies specific for it. The present polypeptide
is useful for generating antibodies specific for it. The present sequence
is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
for this patent did not form part of the printed specification, but was
obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030073623
XX SQ Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 3.05e-105 Length: 476
Score: 107.00 Matches: 107
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 9 Gaps: 0
US-09-541-462B-2 (1-108) x ACH29979 (1-476)
Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 75 GCGGACGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGC 134
Qy 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn 41
Db 135 TTTGAAGTGAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATAAC 194
Qy 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
Db 195 TGTGCCATCTGCAGAACCAACATATGATCTTTGCATAGATGTCAAGCTAACCGCGC 254
Qy 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
Db 255 TCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTC 314
Qy 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrp 101
Db 315 CACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGTGG 374
Qy 102 GluPheGlnLysTyrGlyHis 108
Db 375 GAATTCAAAAGTATGGGCAC 395
RESULT 10
ADS0913/c
ID ADS0913 standard; DNA; 3726 BP.
XX AC ADS0913;
XX 16-DEC-2004 (first entry)
XX Human therapeutic DNA - SEQ ID 150.
XX antiinflammatory; neuroprotective; antianemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX Homo sapiens.

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XX WO2004080148-A2.
XX AC
XX 23-SEP-2004.
XX DT
XX 30-SEP-2003; 2003WO-US030720.
XX DE
XX PF
XX 02-OCT-2002; 2002US-0416186P.
XX KW
XX PR
XX PA
XX (NUVE-) NUVELO INC.
XX PI
XX Tang YT, Asundi V, Ren P, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
XX DR
XX P-PSDB; ADS10597.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 1; SEQ ID NO 150; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic DNA of
XX the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.
XX
XX Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
XX SQ
Alignment Scores:
Pred. No.: 2,43e-103 Length: 3726
Score: 106.00 Matches: 106
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 98.1% Indels: 0
DB: 13 Gaps: 0
US-09-541-462B-2 (1-108) x ADS09913 (1-3726)
Qy 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
Db 492 GCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCGGCAAGCGCTTT 433
Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCys 42
Db 432 GAAAGTGAAGAAGTGAATGAGTACCTCTGGCGCTGGGATATTGGTTGATAACTGT 373
Qy 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
Db 372 GCCATCTCGAGGAACCAATTATGGATCTTTGCTAGATGCTCAAGCTAACCGCGTCC 313
Qy 63 AlatrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 82
Db 312 GCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 253
Qy 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
Db 252 TGCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACAGAGATGGAA 193
Qy 103 PheGlnLysTyrGlyHis 108
Db 192 TTCCAAAAGTATGGGCAC 175
RESULT 11
ACN90161/c
ID ACN90161 standard; DNA; 4543 BP.
```

```
XX ACN90161;
XX AC
XX 02-DEC-2004 (first entry)
XX DT
XX Breast cancer related marker, seq id 11311.
XX DE
XX KW
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX OS
XX Homo sapiens.
XX PN
XX US2003099974-A1.
XX PD
XX 29-MAY-2003.
XX PF
XX 18-JUL-2002; 2002US-00198846.
XX PR
XX 18-JUL-2001; 2001US-0306220P.
XX PA
XX (MILL-) MILLENNIUM PHARM INC.
XX PI
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2003-787014/74.
XX DR
XX Novel isolated polypeptide associated with breast cancer, useful for
XX detecting presence of polypeptide in sample, as a marker for breast
XX cancer.
XX PS
XX Disclosure; SEQ ID NO 11311; 36pp; English.
XX
XX The invention relates to an isolated polypeptide (I) associated with
XX breast cancer which is encoded by a nucleic acid molecule comprising a
XX nucleotide sequence (S1). Further disclosed is an antibody that binds to
XX the polypeptide of the invention. The activity of the polypeptide of the
XX invention may be described as cytostatic. The antibody is useful for
XX detecting the presence of (I) in a sample. Nucleic acid molecules of the
XX invention are useful in the detection of breast tumours. (I) is useful as
XX a marker for breast cancer and in breast cancer therapy. Sequences given
XX in records ACN78851-ACN92934 represent nucleic acid markers associated
XX with breast cancer. Note: The sequence listing does not form part of the
XX specification but may be obtained in electronic format from the USPTO web
XX site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
XX Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
XX SQ
Alignment Scores:
Pred. No.: 2,93e-103 Length: 4543
Score: 106.00 Matches: 106
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 98.1% Indels: 0
DB: 11 Gaps: 0
US-09-541-462B-2 (1-108) x ACN90161 (1-4543)
Qy 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
Db 1085 GCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCGGCAAGCGCTTT 1026
Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCys 42
Db 1025 GAAAGTGAAGAAGTGAATGAGTACCTCTGGCGCTGGGATATTGGTTGATAACTGT 966
Qy 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
Db 965 GCCATCTCGAGGAACCAATTATGGATCTTTGCTAGATGCTCAAGCTAACCGCGTCC 906
Qy 63 AlatrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 82
Db 905 GCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 846
Qy 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
```


||||| 845 TCATCTTCGCTCGCTCAAAACACGACAGGAGTGTGTCATTGGACACAGAGTGGGAA 786

QY 103 PheGlnLysTyrGlyHis 108
|||||
Db 785 TTCCAANAAGTATGGGCAC 768

RESULT 12
ADQ92179
ID ADQ92179 standard; DNA; 503 BP.

AC ADQ92179;
XX
DT 07-OCT-2004 (first entry)

XX Human autoantigen DNA fragment MPMGP800L05536.
XX ds; autoantigen; antibody; hybridoma; biosensor chip;
KW extracorporeal differential diagnosis; autoimmune disease;
KW ribosomal protein; tubulin;
KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
KW affinity chromatography; electrophoresis; autoantibody apheresis;
KW RNA interference; RNAi.

XX Homo sapiens.
OS
XX WO2004058972-A1.
XX
XX 15-JUL-2004.

XX 23-DEC-2002; 2002WO-EP014731.
XX
XX 23-DEC-2002; 2002WO-EP014731.

XX (THIE/) THIESEN H.
XX (LORE/) LORENZ P.
XX Thiesen H, Lorenz P;
XX WPI; 2004-543459/52.

XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic
PT reagents and for treating autoimmune disease, also related expression
PT products and antibodies with similar uses.
XX
XX Claim 1; SEQ ID NO 160; 110pp; German.

XX This invention describes novel human DNA autoantigens which are used to
CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;
CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express
CC monoclonal Ab; biosensor chips having an addressable sequence pattern as
CC probes; medical or diagnostic instruments that include the biosensor; for
CC extracorporeal differential diagnosis of autoimmune diseases and
CC predilection to them. The autoantigen polynucleotides encode ribosomal
CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl
CC transferases and proteins. The antibodies may be labelled conventionally
CC with radioisotopes, coloured or fluorescent groups, or a member of the
CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed
CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear
CC membrane; neurophilin/cytoplasm; insect cells; epidermal intracellular
CC or basal membrane antigens; Golgi or cell nuclei, or associated with
CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope
CC mapping; in affinity chromatography or electrophoresis; for diagnosis,
CC prognosis, control of treatment or therapeutic response of autoimmune
CC diseases, particularly in vitro differential diagnosis of autoimmune
CC diseases; to produce biosensor chips or for autoantibody apheresis.
CC Autoantigen DNA can be used for therapeutic RNA interference against
CC autoantibodies. Biochips that carry the new materials are useful in
CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
XX autoantigens.

XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.47e-103 Length: 503
Score: 105.00 Matches: 105
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.2% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ92179 (1-503)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
Db 3 GCGATGGATGTGGATACCCCGAGCGGCCAACACAGCGCGGCAAGACGCTTTTGA 62
QY 24 VallyLysTyrTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
Db 63 GTGAANAAGTGGATGCGATGAGCCCTCTGGCCCTGGGATATGTGTTGATAACTGTGCC 122
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
Db 123 ATCTGCAGGAACCACTATGATCTTTGCAATGATGCTCAAGCTAACCCAGCGTCCGCT 182
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCys 83
Db 183 ACTTCAGAAGAGTGTACTGTGCGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACTGC 242
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
Db 243 ATCTCTCGTGGCTCAAAACACAGACAGGTGTGTCATTTGGCAACAGAGTGGGAATTC 302
QY 104 GlnLysTyrGlyHis 108
Db 303 CAAAAGTATGGGCAC 317

RESULT 13

AAH97860
ID AAH97860 standard; DNA; 539 BP.
XX
AC AAH97860;
XX
DT 10-OCT-2001 (first entry)
XX
DE Murine 7-transmembrane G-protein coupled receptor coding sequence #104.
XX
KW Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;
KW 7-transmembrane G-protein coupled protein receptor; ds.
XX
XX Mus sp.
XX OS
XX WO200160999-A1.
XX
XX 23-AUG-2001.
XX
XX 14-FEB-2001; 2001WO-US004700.
XX
XX 14-FEB-2000; 2000US-0182377P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR, Witte L, Pereira DS;
XX
XX WPI; 2001-522596/57.
XX
XX DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX
XX Claim 1; Page 62; 176pp; English.
XX
XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The


```

XX 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5119-5120; 11750pp; English.
XX
XX The invention relatés to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	4.75e-100	Length:	4476
Score:	103.00	Matches:	103
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	95.4%	Indels:	0
DB:	5	Gaps:	0

US-09-541-462B-2 (1-108) x ABV25615 (1-4476)

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Qy 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
Db 1014 GCAGCGATGGATGTGGATACCCCGAGCGGACCAACAGCGCGGGCAAGAGCGCTTT 955
Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAlaTrpAspIleValValAspAsnCys 42
Db 954 GAAGTGAANAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGT 895
Qy 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
Db 894 GCCATCTGCAGAACCAACATTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGCGCTCC 835
Qy 63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82
Db 834 GCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 775
Qy 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
Db 774 TGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCTCATTTGGACACAGAGAGTGGAA 715
Qy 103 PheGlnLys 105
Db 714 TTCCAAAAA 706

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Search completed: March 11, 2006, 09:53:11
Job time : 501 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:27:10 ; Search time 349 Seconds

(without alignments)
714.006 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMVDVPTSGTNSGAGK.....KTRQVCLDNREWFQKYGH 108

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ASSWEB_spool/US09541462/runat_10032006_080737_22172/app_query.fasta_1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOFCU=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsu62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs05h
-USER=US09541462 -CGN_1_1_431 -runat_10032006_080737_22172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	85.6	660	9	US-11-096-568A-11809 Sequence 11809, A
2	516.5	83.8	432	9	US-11-096-568A-14405 Sequence 14405, A
3	515.5	83.7	693	9	US-11-096-568A-26820 Sequence 26820, A
4	499	81.0	348	9	US-11-096-568A-28569 Sequence 28569, A

5	385	62.5	366	7	US-10-932-182A-78459 Sequence 78459, A
6	385	62.5	366	7	US-10-932-182A-78459 Sequence 78459, A
7	381	61.9	366	7	US-10-932-182A-2279 Sequence 2279, Ap
8	381	61.9	366	7	US-10-932-182A-2279 Sequence 2279, Ap
9	292	47.4	342	8	US-10-821-234-554 Sequence 554, App
10	234	38.0	546	12	US-11-128-061-5740 Sequence 5740, Ap
11	234	38.0	546	12	US-11-128-049-5740 Sequence 5740, Ap
12	234	38.0	579	12	US-11-128-061-2098 Sequence 2098, Ap
13	234	38.0	579	12	US-11-128-049-2098 Sequence 2098, Ap
14	217	35.2	648	5	US-09-978-360A-4 Sequence 4, Appl
15	215	34.9	450	9	US-11-057-484A-14 Sequence 14, Appl
16	211	34.3	3404	12	US-11-045-468A-18 Sequence 18, Appl
c 17	196	31.8	153	7	US-10-932-182A-81177 Sequence 81177, A
c 18	196	31.8	153	7	US-10-932-182A-81177 Sequence 81177, A
c 19	195	31.7	420	8	US-10-821-234-360 Sequence 360, App
c 20	175	28.4	207	7	US-10-932-182A-6146 Sequence 6146, Ap
c 21	175	28.4	207	7	US-10-932-182A-6146 Sequence 6146, Ap
c 22	137.5	22.3	2135	9	US-11-072-512-459 Sequence 459, App
23	133	21.6	498	7	US-10-932-182A-75906 Sequence 75906, A
24	133	21.6	498	7	US-10-932-182A-75906 Sequence 75906, A
25	99	16.1	2027	9	US-11-096-568A-12921 Sequence 12921, A
26	95.5	15.5	752	9	US-11-096-568A-3548 Sequence 3548, Ap
27	95	15.4	922	9	US-11-096-568A-13533 Sequence 13533, A
28	93	15.1	808	9	US-11-096-568A-1239 Sequence 1239, Ap
29	91	14.8	76	8	US-10-310-914A-128 Sequence 128, App
30	91	14.8	76	8	US-10-310-914A-16478 Sequence 16478, A
31	91	14.8	683	9	US-11-096-568A-3705 Sequence 3705, Ap
32	91	14.8	1324	9	US-11-096-568A-3994 Sequence 3994, Ap
33	89.5	14.5	908	9	US-11-096-568A-5433 Sequence 5433, Ap
34	89	14.4	849	9	US-11-096-568A-21222 Sequence 21222, A
35	89	14.4	1107	9	US-11-087-099-132 Sequence 132, App
36	88	14.3	1976	9	US-11-072-512-1680 Sequence 1680, Ap
37	87	14.1	1250	9	US-11-096-568A-23080 Sequence 23080, A
38	86.5	14.0	615	9	US-11-096-568A-730 Sequence 730, App
39	86	14.0	791	9	US-11-096-568A-20676 Sequence 20676, A
40	86	14.0	2008	8	US-10-955-054A-150 Sequence 150, App
41	85.5	13.9	1479	9	US-11-096-568A-6605 Sequence 6605, Ap
42	85.5	13.9	2138	9	US-11-096-568A-11058 Sequence 11058, A
43	85	13.8	3599	12	US-11-080-991-39 Sequence 39, Appl
44	84.5	13.7	1287	9	US-11-096-568A-24773 Sequence 24773, A
45	84	13.6	362	7	US-10-991-285-134 Sequence 134, App

ALIGNMENTS

RESULT 1
US-11-096-568A-11809
; Sequence 11809, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11809
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 13657464
US-11-096-568A-11809

Alignment Scores:	1.97e-49	Length:	660
Pred. No.:	527.00	Matches:	94
Score:	79.8%	Conservative:	5
Best Local Similarity:	75.8%	Mismatches:	7
Query Match:	85.6%	Indels:	18


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QY 19 -----LysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
Db 82 GTGAAACAAAGAGAGATTGAAATTAAGAAATGGACCCAGTGGCGTTTGGTCA 141
QY 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
Db 142 TGGGATATAGCTGTTGACACACTGCTATTGTCAGGAACCATATATGGAACCATGCATT 201
QY 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyVal 74
Db 202 GAATGCCAGCAAGGCCATGACGACACTGATAATGAATGTTGTAGCAGCTGGGTGTC 261
QY 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94
Db 262 TGAATACACCTTTCCATTGCACTGTATTAAATAAATGATCAAGACAGACGACGATGC 321
QY 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 322 CCATTAGATTAACCACTTGGCAGTTAGCAAGATGCGGT 360

```

RESULT 7

```

US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

```

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Alignment Scores:
Pred. No.: 2,25e-33 Length: 366
Score: 381.00 Matches: 62
Percent Similarity: 73.0% Conservative: 11
Best Local Similarity: 62.0% Mismatches: 23
Query Match: 61.9% Indels: 4
DB: 7 Gaps: 1

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US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

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QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrp 27
Db 73 AATACACCGGTAGACACAA-----AAAAAAGATTCCAGATTAAATAATGG 120
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
Db 121 ACAGCGGTGGCGTTCTGCTGGGTATATAGCCGTTGACAACTGTGCCATTGCGAAGAAC 180
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67
Db 181 CACATTATGGAACCATGCATCGAATGCCCGGCTATGACCGGACACAGATAACGAA 240
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87
Db 241 TGTGTGCAGACATGGGTGTTGTAATACCGCTTTCACCTTGCACTGCATCAATAATGG 300
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 301 ATCAAGACGAGATGTCATGCCCTTGGACAAACCACTTGGCAATTGGCAAGTGGCGGT 360

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RESULT 8

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US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

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Alignment Scores:
Pred. No.: 2,25e-33 Length: 366
Score: 381.00 Matches: 62
Percent Similarity: 73.0% Conservative: 11
Best Local Similarity: 62.0% Mismatches: 23
Query Match: 61.9% Indels: 4
DB: 7 Gaps: 1

```

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

```

QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrp 27
Db 73 AATACACCGGTAGACACAA-----AAAAAAGATTCCAGATTAAATAATGG 120
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
Db 121 ACAGCGGTGGCGTTCTGCTGGGTATATAGCCGTTGACAACTGTGCCATTGCGAAGAAC 180
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67
Db 181 CACATTATGGAACCATGCATCGAATGCCCGGCTATGACCGGACACAGATAACGAA 240
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87
Db 241 TGTGTGCAGACATGGGTGTTGTAATACCGCTTTCACCTTGCACTGCATCAATAATGG 300
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 301 ATCAAGACGAGATGTCATGCCCTTGGACAAACCACTTGGCAATTGGCAAGTGGCGGT 360

```

RESULT 9

```

US-10-821-234-554
; Sequence 554, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 554
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-554

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Alignment Scores:

Pred. No.: 1,966-23 Length: 342
Score: 292.00 Matches: 49
Percent Similarity: 64.9% Conservative: 14
Best Local Similarity: 50.5% Mismatches: 30
Query Match: 47.4% Indels: 4
DB: 8 Gaps: 2

US-09-541-462B-2 (1-108) x US-10-821-234-554 (1-342)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysTrpAsnAlaVal 30
Db 58 TCAGCTCCAAAGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACGCGTC 114
Qy 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 115 GCCATGTGGAGCTGGAGCTGGAGTCGATACGTGCGCCATCTGCAGGTCAGGTGATG 174
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 175 GATGCTGCTTAGATGTCAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 226 GTCTGGGGAGAATGTAATCATCTCTCCACAACACTGCTGCATGCTCCCTGTGGTGAACAG 285
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyGly 107
Db 286 AACAAATCGCTGCTCTCTGTCACAGGAGGACTGGGTGTCACAAAGAATCGGC 336

RESULT 10

US-11-128-061-5740
; Sequence 5740, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5740
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t

US-11-128-061-5740
Alignment Scores:
Pred. No.: 1,07e-16 Length: 546
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-061-5740 (1-546)
Alignment Scores:
Pred. No.: 1,07e-16 Length: 546
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-061-5740 (1-546)

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Db 50 GCGGCTCCAAAGTCGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACGCGTA 106
Qy 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATGCTGCTCAGATGTCAGCGCAAAAC-----AAACAAGAGGACTGTGTTGTG 217
Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 218 GTCTGGGGAGAATGTAATCATCTCTCCACAACACTGCTGCATGCTCTGTGGTGAACAG 277
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyGly 107
Db 278 AACAAATCGCTGCTCTCTGTCACAGGAGGACTGGGTGTCACAAAGAATTTGGC 328

RESULT 11

US-11-128-049-5740
; Sequence 5740, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5740
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-5740
Alignment Scores:
Pred. No.: 1,07e-16 Length: 546
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-049-5740 (1-546)
Alignment Scores:
Pred. No.: 1,07e-16 Length: 546
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysTrpAsnAlaVal 30
Db 50 GCGGCTCCAAAGTCGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACGCGTA 106
Qy 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATGCTGCTCAGATGTCAGCGCAAAAC-----AAACAAGAGGACTGTGTTGTG 217

QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysThrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 12
US-11-128-061-2098
; Sequence 2098, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2098
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (547)..(568)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-2098

Alignment Scores:
Pred. No.: 1,15e-16 Length: 579
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-061-2098 (1-579)

QY 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysLysTrpAsnAlaVal 30
Db 50 GCGGGCTCCAAGTCGGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACGCGTA 106
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166

QY 51 AspLeuValGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATCGCTCCCTCAGATGTCAGCCGAAAC-----AAACAAGAGGACTGTGTGTG 217

QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277

QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysThrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 14
US-09-978-360A-4
; Sequence 4, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:

Db 278 AACAAATCGCTGCTCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 13
US-11-128-049-2098
; Sequence 2098, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2098
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (547)..(568)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-2098

Alignment Scores:
Pred. No.: 1,15e-16 Length: 579
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-049-2098 (1-579)

QY 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysLysTrpAsnAlaVal 30
Db 50 GCGGGCTCCAAGTCGGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACGCGTA 106
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166

QY 51 AspLeuValGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATCGCTCCCTCAGATGTCAGCCGAAAC-----AAACAAGAGGACTGTGTGTG 217

QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277

QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysThrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 14
US-09-978-360A-4
; Sequence 4, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.USA.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 648
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 187..438
FEATURE:
NAME/KEY: polyA signal
LOCATION: 612..617
FEATURE:
NAME/KEY: polyA site
LOCATION: 632..648
US-09-978-360A-4
Alignment Scores:
Pred. No.: 1.06e-14 Length: 648
Score: 217.00 Matches: 43
Percent Similarity: 44.5% Conservative: 18
Best Local Similarity: 31.4% Mismatches: 40
Query Match: 35.2% Indels: 36
DB: 5 Gaps: 3
US-09-541-462B-2 (1-108) x US-09-978-360A-4 (1-648)
Qy 2 AlaalaMetaspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 49 GCGCGGAGTGTGGTCTTTTATACCTTCCCGCGGACGCCGCGCTGCCAACGGAAG 108
Qy 22 PheGlu-----ValLysLysTrpAsnAlaValAlaLeuTrp 33
Db 109 GCGGAGAGGAGTTTCGTGTCATGTTGGCCAGGCCCATTTGAGATCTTTGAGATATCTCA 168
Qy 24 -----ValLysLysTrpAsnAlaValAlaLeuTrp 33
Db 169 ACGTGAGGCTCTGCTGCATCAAGGTGAAGTTAAGTCTGGAACGCGGTGGCACTTG 228
Qy 34 AlaTrpAspLeuValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
Db 229 CTCCTGGTGCCCAACGATGAGAACTGTGGCATCTGCAGGATGTCATTTAAACGGATGCTGC 288

Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 289 CCTGACTGCAAG-----GTCCCGGCGACGACTGCCCGCTGGTGGGCGC 333
Qy 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 334 CAGTGCTCCCACTGCTTCCCATGTCATCTCAAGTGGCTGCGACGACGACGAGTG 393
Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 394 CAGCAGCAGTGCCTCCCATGTCGCCCGCAGGAGTGAAGTTCAAGGAGTGAGGC 444
RESULT 15
US-11-057-484A-14
Sequence 14, Application US/11057484A
Publication No. US20060029931A1
GENERAL INFORMATION:
APPLICANT: Finkel, Terri H.
APPLICANT: Yin, Jiyl
TITLE OF INVENTION: Cellular Genes Regulated by HIV-1
FILE REFERENCE: CHOP.0146CIP
CURRENT APPLICATION NUMBER: US/11/057,484A
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: US 10/368,803
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/358,495
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 450
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: n = A, C, G or T
US-11-057-484A-14
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Pred. No.: 1.15e-14 Length: 450
Score: 215.00 Matches: 41
Percent Similarity: 53.6% Conservative: 11
Best Local Similarity: 42.3% Mismatches: 23
Query Match: 34.9% Indels: 23
DB: 9 Gaps: 2
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Db 54 TCAGGCTCCAGTCCGGA---GGCGACAGATGTTTCTCCCAAGAGTGGACGCGGTG 110
Qy 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 111 GCCATGTGGAGCTGGGACGCGGAGTGGAGTACGTGCGCCATCTGCAGGT----- 160
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 161 -----CCAGTG 166
Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 167 GTCTGGGGAGATGATGATCATCTCTTCCCAACTGCTGTCATGCTCCCTGGTGGGTAACAG 226
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 227 AACAACTGNTGCCCTCTCTGCCAGCAGGAGTGGTGGTCCAAAGATCGGC 277
Search completed: March 11, 2006, 08:43:57
Job time : 352 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:13:49 ; Search time 134 Seconds
(without alignments)
1432.662 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVTPSGTNSGAGKK.....KTRQVCLDNRWFQYKXH 108

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	616	100.0	508	3	US-09-914-324A-3
5	501.5	81.4	3208	3	US-09-780-016-27
6	501.5	81.4	3208	3	US-10-214-811-27
7	501.5	81.4	3208	3	US-10-766-074-27
8	479	77.8	411	3	US-09-640-211A-1731
9	400.5	65.0	490	3	US-09-270-767-26812

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	11	394	64.0	402	3	US-09-513-999C-10371	Sequence 10371, A
	12	394	64.0	463	3	US-09-621-976-15180	Sequence 15180, A
	13	385	62.5	480	3	US-09-914-324A-4	Sequence 4, Appli
	14	375.5	61.0	357	3	US-09-248-796A-5495	Sequence 5495, Ap
	15	287	46.6	342	3	US-09-826-312A-7	Sequence 7, Appli
	16	287	46.6	342	3	US-09-542-497A-7	Sequence 7, Appli
	17	287	46.6	342	3	US-10-108-767-7	Sequence 7, Appli
	18	262.5	42.6	301	3	US-09-313-294A-492	Sequence 492, App
	19	217	35.2	648	3	US-09-599-360B-27	Sequence 27, Appl
	20	200.5	32.5	534	3	US-09-621-976-1817	Sequence 1817, Ap
	21	198	32.1	671	3	US-09-621-976-1854	Sequence 1854, Ap
	22	197.5	32.1	539	3	US-09-621-976-2051	Sequence 2051, Ap
	23	191	31.0	654	3	US-09-621-976-1945	Sequence 1945, Ap
	24	175	28.4	25274	3	US-09-949-016-16682	Sequence 16682, A
	25	173	28.1	585	3	US-09-270-767-10788	Sequence 10788, A
	26	150.5	24.4	439	3	US-09-799-451-296	Sequence 296, App
	27	146	23.7	170	3	US-09-270-767-26253	Sequence 26253, A
	28	137.5	22.3	2135	3	US-10-104-047-459	Sequence 459, App
	29	91	14.8	940	3	US-09-023-655-667	Sequence 667, App
	30	91	14.8	1839	3	US-09-828-303-10	Sequence 10, Appl
	31	90	14.6	872	3	US-09-774-528-304	Sequence 304, App
	32	90	14.6	872	3	US-10-120-988-304	Sequence 304, App
	33	90	14.6	893	3	US-09-949-016-4980	Sequence 4980, Ap
	34	90	14.6	1690	3	US-09-828-303-2	Sequence 2, Appli
	35	90	14.6	3140	3	US-09-774-528-255	Sequence 255, App
	36	90	14.6	3140	3	US-10-120-988-255	Sequence 255, App
	37	90	14.6	8438	2	US-07-945-283-1	Sequence 1, Appli
	38	88	14.3	1183	3	US-09-799-451-763	Sequence 763, App
	39	88	14.3	1976	3	US-10-104-047-1680	Sequence 1680, Ap
	40	86	14.0	363	3	US-09-640-211A-1319	Sequence 1319, Ap
	41	86	14.0	1267	3	US-09-949-016-378	Sequence 378, App
	42	86	14.0	1267	3	US-09-949-016-2914	Sequence 2914, Ap
	43	85.5	13.9	3304	3	US-09-799-451-220	Sequence 220, App
	44	85	13.8	1621	3	US-03-023-655-20	Sequence 20, Appl
	45	85	13.8	1995	3	US-09-949-016-3134	Sequence 3134, Ap

ALIGNMENTS

RESULT 1

US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29...352
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 401
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 404
; OTHER INFORMATION: m-a or c
US-09-513-999C-3894

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Alignment Scores:
Pred. No.: 1.48e-66 Length: 482
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 29 ATGGCGCGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 88
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 89 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 149 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATG 208
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 209 GCGTCCGCTACTTCCAGAGAGTGTACTGTCCGATGGGAGTGTCTGAACCATGCTTTTC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 269 TTCACATGCAATCTCTCGCTGGCTCAAAACAGCAGCAGGTGTCTCAATGGACACAGAG 328
QY 101 TrpGluPheGlnLysTyrGlyHis 108
Db 329 TGGGAATTCCAAAAGTATGGGCAC 352

RESULT 2
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Alignment Scores:
Pred. No.: 1.57e-66 Length: 504
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGCGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATG 186

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Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaLysThrGlyValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCACATGCACTCTCTCGCTGGCTTAAACACACGACAGGTGTGTCTCATTTGGACACAGAG 306
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 307 TGGGAATTCCAAAGATATGGGCAC 330
RESULT 4
US-09-914-324A-3
; Sequence 3, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; TITLE OF INVENTION: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-09-914-324A-3
Alignment Scores:
Pred. No.: 1.58e-66 Length: 508
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-09-541-462B-2 (1-108) x US-09-914-324A-3 (1-508)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGCGCGCAGCGATGGATGTGATACCCCGCGGCGCACCAACGCGCGCGGCAAGAG 66
Qy 21 ArgPheGluValLysLysThrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 67 CGCTTTGAGTGAAGTGAATGCAAGTAGCCCTCTGGGCTGGGATATTTGGTTGAT 126
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACGTGTCATCTCGAGGACCAACATTTATGATCTTTGCATAGATGCTAAGCTAACAG 186
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaLysThrArgGlnValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCACATGCACTCTCTCGCTGGCTTAAACACACGACAGGTGTGTCTCATTTGGACACAGAG 306
Qy 101 TrpGluPheGlnLysTyrGlyHis 108

Db 307 TGGGAATTCCAAAGATATGGGCAC 330
RESULT 5
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6509456el Human Proteases and
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27
Alignment Scores:
Pred. No.: 2.1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: 3 Gaps: 1
US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)
Qy 16 GlyAlaGlyLysLysArgPheGluValLysThrAsnAlaValAlaLeuTrpAlaTrp 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATCAGTAGCCCTCTGGGCTGG 2802
Qy 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGTGTGATTAACGTGTCATCTGCAGAACACACATTATGGATCTTTGCATAGAA 2862
Qy 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaLysGlyValCys 75
Db 2863 TGTCAAGCTAACCCAGCGCTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGT 2922
Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTyrLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTTCATCTCCATCTCTCGCTGGCTCAAAACACACAGAGGTGTGTGCCA 2982
Qy 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 2983 TTGACACACAGAGTGGGAATTCCAAAGATATGGGCAC 3021
RESULT 6
US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6743621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743621el Human Proteases and

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; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-214-811-27

Alignment Scores:
Pred. No.: 2,1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: Gaps: 1

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

QY 16 GlyAlaGlyLysIysArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrp 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATGCAGTAGCCCTCTGGGCTGG 2802

QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGGTTGATTAACCTGTCATCTGCAGAACACACATTATGGATCTTTGCATAGAA 2862

QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
Db 2863 TGTCAAGCTAACACAGCGCTCCGCTACTTCAAGAGAGTGTACTGTGCGATGGGAGTCTGT 2922

QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCA 2982

QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 2983 TTGGACACACAGAGTGGGAATTCCAAAGTATGGGCAC 3021

RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/766,074
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208

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; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-074-27

Alignment Scores:
Pred. No.: 2,1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: Gaps: 1

US-09-541-462B-2 (1-108) x US-10-766-074-27 (1-3208)

QY 16 GlyAlaGlyLysIysArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrp 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATGCAGTAGCCCTCTGGGCTGG 2802

QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGGTTGATTAACCTGTCATCTGCAGAACACACATTATGGATCTTTGCATAGAA 2862

QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
Db 2863 TGTCAAGCTAACACAGCGCTCCGCTACTTCAAGAGAGTGTACTGTGCGATGGGAGTCTGT 2922

QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCA 2982

QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 2983 TTGGACACACAGAGTGGGAATTCCAAAGTATGGGCAC 3021

RESULT 8
US-09-640-211A-1731
; Sequence 1731, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(411)
; OTHER INFORMATION: n = A,T,C or G
; US-09-640-211A-1731

Alignment Scores:
Pred. No.: 7,79e-50 Length: 411
Score: 479.00 Matches: 90
Percent Similarity: 85.0% Conservative: 6
Best Local Similarity: 79.6% Mismatches: 4
Query Match: 77.8% Indels: 13
DB: Gaps: 3

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)

QY 3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerGlyAla 17
Db 74 GCTTCAACACACATAGATATGATTCGCGTGCCTCTGGCGAGGGTTCAGCTCTCAAGCG 133

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Qy 18 Gly-----LysLysArgPheGluValLysLysValLysLysValLysLysVal 30
 Db 134 GGACCAAGCGCTTCACCAAGAGCCAAAGCTTTGGAATCAAGAACTGCAATGCTGTA 193
 Qy 31 AlaLeuTrpAlaTrpAspLysValValAspLysValLysLysValLysLysVal 50
 Db 194 GCCCTTTGGCGTGGATATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 253
 Qy 51 AspLeuValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 70
 Db 254 GACCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 313
 Qy 71 AlaTrpGluValCysAsnHisAlaPheHisCysLysLysLysLysLysLysLys 90
 Db 314 GCATGGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 373
 Qy 91 ArgGlnValCysProLeuAspAsnArg-GluTrpGlu 102
 Db 374 CGACAAAGTCTGCCATTAGATAAATAGTGGAG 410

RESULT 9

US-09-270-767-26812/c
 ; Sequence 26812, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 26812
 ; LENGTH: 490
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-26812

Alignment Scores:
 Pred. No.: 4,25e-40 Length: 490
 Score: 400.50 Matches: 70
 Percent Similarity: 77.6% Conservatives: 13
 Best Local Similarity: 65.4% Mismatches: 19
 Query Match: 65.0% Indels: 5
 DB: 3 Gaps: 2
 US-09-541-462b-2 (1-108) x US-09-270-767-26812 (1-490)

Qy 5 MetAspValAspThrProSerGlyThrAsnSerGly-----AlaGlyLysLys 20
 Db 370 ATGGACTTCATGACGAGAGCCATCTGTAGTGGAGAGCTGTCCAGGCAGGAG 311
 Qy 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
 Db 310 CGCTTTGGTGGTGAAGAAATGGTTGCGCAGCCATGTGGGATGGGACGTAGCAGTGAC 251
 Qy 41 AsnCysAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
 Db 250 AACTGTGCCATCTCCGCTAACCAATCATGATGATGATGATGATGATGATGATGATGAT 194
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 193 CCGAATGCAACCAAGAGAGTGCATGTGCTTGGGGGAGTGCACCAACGATTCAT 134
 Qy 81 PheHisCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 100
 Db 133 TACCACTGCATCGCGCGTGGTTGAAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 74
 Qy 101 TrpGluPheGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 107
 Db 73 TGGGTCTACCAAGAGTACGGC 53

RESULT 10

US-09-270-767-11265/c
 ; Sequence 11265, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 11265
 ; LENGTH: 1101
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-11265

Alignment Scores:
 Pred. No.: 1,25e-39 Length: 1101
 Score: 400.50 Matches: 70
 Percent Similarity: 77.6% Conservatives: 13
 Best Local Similarity: 65.4% Mismatches: 19
 Query Match: 65.0% Indels: 5
 DB: 3 Gaps: 2
 US-09-541-462b-2 (1-108) x US-09-270-767-11265 (1-1101)

Qy 5 MetAspValAspThrProSerGlyThrAsnSerGly-----AlaGlyLysLys 20
 Db 981 ATGGACTTCATGACGAGAGCCATCTGTAGTGGAGAGCTGTCCAGGCAGGAG 922
 Qy 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
 Db 921 CGCTTTGGTGGTGAAGAAATGGTTGCGCAGCCATGTGGGATGGGACGTAGCAGTGAC 862
 Qy 41 AsnCysAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
 Db 861 AACTGTGCCATCTCCGCTAACCAATCATGATGATGATGATGATGATGATGATGATGAT 805
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 804 CCGAATGCAACCAAGAGAGTGCATGTGCTTGGGGGAGTGCACCAACGATTCAT 745
 Qy 81 PheHisCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 100
 Db 744 TACCACTGCATCGCGCGTGGTTGAAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 685
 Qy 101 TrpGluPheGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 107
 Db 684 TGGGTCTACCAAGAGTACGGC 664

RESULT 11

US-09-513-999C-10371
 ; Sequence 10371, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pn
 ; SEQ ID NO 10371
 ; LENGTH: 402
 ; TYPE: DNA
 ; ORGANISM: *Homo sapiens*

QY 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGly----- 18
DB 25 ATGGATGTTGATGAAGATGAATCGCAAAATATTCGCAAAAGCTCAAAACAAAGTGCGCCA 84
QY 19 -----LysLeuArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
DB 85 GTGGAAACCAAAAGAGAGATTGAAATTAAGAATGAGCGCGATGCGTTTGGTCA 144
QY 35 TrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
DB 145 TGGGATATAGCTGTTGCAACACTGTCTATTTGCAGGAACCATATAATGGAACCATGCATT 204
QY 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyVal 74
DB 205 GAATGCCAGCCAAAGCCCATGACGACACTGATAATGAATGTAGCAGCGCTGGGGTGC 264
QY 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94
DB 265 TGTATACAGCTTTCCATTGCACTGTATTAATTAATGATCAAGACAAGAGACGATGC 324
QY 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
DB 325 CCATTAGATAACCAACCTTGGCAGTTAGCAAGATCGCGT 363
RESULT 14
US-09-248-796A-5495
; Sequence 5495, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5495
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5495
Alignment Scores:
Pred. No.: 3,26e-37 Length: 357
Score: 375.50 Matches: 62
Percent Similarity: 73.3% Conservative: 12
Best Local Similarity: 61.4% Mismatches: 26
Query Match: 61.0% Indels: 1
DB: 3 Gaps: 1
US-09-541-462B-2 (1-108) x US-09-248-796A-5495 (1-357)
QY 9 ThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsn 28
DB 52 ACAACAGAACCAATCAAAACCATCATCAAAACCAAGATTGAAGTGAAGAAATGACA 111
QY 29 AlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHis 48
DB 112 GCGGTAGCGTTTGGTTCATGGATATGCAAAATGCAAAATGTCGCAATTTGTAGAAATCAT 171
QY 49 IleMetAspLeuCysIleGluCysGlnAlaAsn---GlnAlaSerAlaThrSerGluGlu 67
DB 172 TTAATGGAACCATGATTATGAATGCAACCAATGCTATGGGTATATATTCCTTCAGAAAG 231
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrp 87
DB 232 TGTATTCCTGCTGGGAGATGATGAATCATGTCATTTTACATTTGATTTAGAAAGATGG 291
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107

DB 292 TTGAAAAACAAGAAATGCAATGCTCCCTTGGATAGTACTAATTGCACTTATCAAAAAATTGGGT 351
QY 108 His 108
DB 352 AAT 354
RESULT 15
US-09-826-312A-7
; Sequence 7, Application US/09826312A
; Patent No. 6737244
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/09/826,312A
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: RING finger protein ROC2
US-09-826-312A-7
Alignment Scores:
Pred. No.: 2,24e-26 Length: 342
Score: 287.00 Matches: 48
Percent Similarity: 63.9% Conservative: 14
Best Local Similarity: 49.5% Mismatches: 31
Query Match: 46.6% Indels: 4
DB: 3 Gaps: 2
US-09-541-462B-2 (1-108) x US-09-826-312A-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
DB 58 TCAGGCTCAACGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGAACCCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHisIleMet 50
DB 115 GCCATGTGGAGCTGGGACGTGGAGTGCATACGTGCGCCATCTGCAGGGTCCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
DB 175 GATGCCCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
DB 226 GTCTGGGAGAAATGTAATCAATTCCTTCCACAACTGCTGCAATGCCCTGTGGTGAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
DB 286 AACAAATCGCTGCCCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGCG 336
Search completed: March 11, 2006, 08:22:43
Job time : 137 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 14:30:51 ; Search time 297.184 Seconds
(without alignments)
2538.786 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgccagcgatggatgt.....tccaaaagtatgggcactag 327

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7673375 seqs, 115364844 residues

Word size : 12

Total number of hits satisfying chosen parameters: 38280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PC7_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	7.6	25	12	US-11-121-849-188861
2	25	7.6	25	12	US-11-121-849-188862
3	25	7.6	25	12	US-11-121-849-188863
4	25	7.6	25	12	US-11-121-849-188864
5	25	7.6	25	12	US-11-121-849-188865
6	25	7.6	25	12	US-11-121-849-188866
7	25	7.6	25	12	US-11-121-849-188867
8	23	7.0	23	12	US-11-090-617-351
9	19	5.8	19	10	US-11-101-244-692822
10	19	5.8	19	10	US-11-101-244-692823
11	19	5.8	19	10	US-11-101-244-692824
12	19	5.8	19	10	US-11-101-244-692826
13	19	5.8	19	10	US-11-101-244-692827
14	19	5.8	19	10	US-11-101-244-692829
15	19	5.8	19	10	US-11-101-244-692830
16	19	5.8	19	10	US-11-101-244-692831
17	19	5.8	19	10	US-11-101-244-692832
18	19	5.8	19	10	US-11-101-244-692833
19	19	5.8	19	10	US-11-101-244-692835
20	19	5.8	19	10	US-11-101-244-692836

ALIGNMENTS

RESULT 1

US-11-121-849-188861
; Sequence 188861, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188861
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188861

RESULT 2

US-11-121-849-188862
; Sequence 188862, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

21	19	5.8	19	10	US-11-101-244-692837	Sequence 692837,
22	19	5.8	19	10	US-11-101-244-692840	Sequence 692840,
23	19	5.8	19	10	US-11-101-244-692841	Sequence 692841,
24	19	5.8	19	10	US-11-101-244-692842	Sequence 692842,
25	19	5.8	19	10	US-11-101-244-692843	Sequence 692843,
26	19	5.8	19	10	US-11-101-244-692844	Sequence 692844,
27	19	5.8	19	10	US-11-101-244-692845	Sequence 692845,
28	19	5.8	19	10	US-11-101-244-692846	Sequence 692846,
29	19	5.8	19	10	US-11-101-244-692848	Sequence 692848,
30	19	5.8	19	10	US-11-101-244-692849	Sequence 692849,
31	19	5.8	19	10	US-11-101-244-692850	Sequence 692850,
32	19	5.8	19	10	US-11-101-244-692852	Sequence 692852,
33	19	5.8	19	11	US-11-083-784-692822	Sequence 692822,
34	19	5.8	19	11	US-11-083-784-692823	Sequence 692823,
35	19	5.8	19	11	US-11-083-784-692824	Sequence 692824,
36	19	5.8	19	11	US-11-083-784-692826	Sequence 692826,
37	19	5.8	19	11	US-11-083-784-692827	Sequence 692827,
38	19	5.8	19	11	US-11-083-784-692829	Sequence 692829,
39	19	5.8	19	11	US-11-083-784-692830	Sequence 692830,
40	19	5.8	19	11	US-11-083-784-692831	Sequence 692831,
41	19	5.8	19	11	US-11-083-784-692832	Sequence 692832,
42	19	5.8	19	11	US-11-083-784-692833	Sequence 692833,
43	19	5.8	19	11	US-11-083-784-692835	Sequence 692835,
44	19	5.8	19	11	US-11-083-784-692836	Sequence 692836,
45	19	5.8	19	11	US-11-083-784-692837	Sequence 692837,

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 AGCGTCCGCTACTTCAGAGAGTG 203

Db 1 AGCGTCCGCTACTTCAGAGAGTG 25

; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188862

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 TCAGAGAGTGTTACTCGCATGGG 217
Db 1 TCAGAGAGTGTTACTCGCATGGG 25

RESULT 3

US-11-121-849-188863
; Sequence 188863, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188863

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCGATCTCTCGTGCTCAAAACA 270
Db 1 CTCGATCTCTCGTGCTCAAAACA 25

RESULT 4

US-11-121-849-188864
; Sequence 188864, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188864

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 TCGCTGGCTCAAAACACGACGAGTG 279

Db 1 TCGCTGGCTCAAAACACGACGAGTG 25

RESULT 5

US-11-121-849-188865
; Sequence 188865, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188865

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 CACGACAGGTGTGTCATTGGACAA 293
Db 1 CACGACAGGTGTGTCATTGGACAA 25

RESULT 6

US-11-121-849-188866
; Sequence 188866, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188866

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 GACAAACAGAGTGGGAATTCCTCAA 313
Db 1 GACAAACAGAGTGGGAATTCCTCAA 25

RESULT 7

US-11-121-849-188867
; Sequence 188867, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188867
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188867

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GGGAAATCCAAAGTATGGGCACTA 326
|||||
Db 1 GGGAAATCCAAAGTATGGGCACTA 25

RESULT 8

US-11-090-617-351
; Sequence 351, Application US/11090617
; Publication No. US20060024692A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Daigo, Yataro
; APPLICANT: Nakatsuru, Shuichi
; TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
; FILE REFERENCE: 082368-003500US
; CURRENT APPLICATION NUMBER: US/11/090,617
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP04/04075
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/JP03/12072
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US 60/555,757
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/466,100
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/451,374
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,673
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 706
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR
US-11-090-617-351

Query Match 7.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GTGAAAAGTGGAAATGCAGTAGC 92
|||||
Db 1 GTGAAAAGTGGAAATGCAGTAGC 23

RESULT 9

US-11-101-244-692822
; Sequence 692822, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692822
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692822

Query Match 5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 53 GCAAGAAGCGCTTTGAAGT 71
|||||
Db 1 GCAAGAAGCGCTTTGAAGT 19

RESULT 10

US-11-101-244-692823
; Sequence 692823, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692823
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692823

Query Match 5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 57 GAAGCGCTTTGAAGTGAAG 75
|||||
Db 1 GAAGCGCTTTGAAGTGAAG 19

RESULT 11

US-11-101-244-692824
; Sequence 692824, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692824

Query Match          5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 104 GGGATATTGGTTGATAA 122
|||||:|:|:|:|:|:|
Db 1 GGGAAUUGGUGGAUAA 19

RESULT 12
US-11-101-244-692826
; Sequence 692826, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692826
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692826

Query Match          5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAGAAGCGCTTGAAGTGA 73
|||||:|:|:|:|:|:|
Db 1 AAGAAGCGCUUGAUGA 19

RESULT 13
US-11-101-244-692827
; Sequence 692827, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692827
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692827

Query Match          5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 291 CAACAGAGAGTGGGAATTC 309
|||||:|:|:|:|:|:|
Db 1 CAACAGAGAGUGGAUUC 19

RESULT 14
US-11-101-244-692829
; Sequence 692829, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692829

Query Match          5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 1.7;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 137 GGAACCAACATTATGGATCT 155
|||||:|:|:|:|:|:|
Db 1 GGAACCACAUAUGGAUCU 19

RESULT 15
US-11-101-244-692830
; Sequence 692830, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692830

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred.No. 1.7;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      134 GCAGGAACCACTTATGGA 152
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Db       1 GCAGGAACCAUUGGA 19

Search completed: March 8, 2006, 14:44:48
Job time : 297.184 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 8, 2006, 13:59:49 ; Search time 536.691 Seconds
(without alignments)
5038.446 Million cell updates/sec

Title: US-09-541-462B-1
Perfect score: 327
Sequence: 1 atggcgagcgatgatgt.....tccaaagtatggcactag 327

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 12

Total number of hits satisfying chosen parameters: 145515

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	433	7	US-10-242-535A-43377
2	327	100.0	433	7	US-10-085-783A-43377
3	327	100.0	453	7	US-10-242-535A-35025
4	327	100.0	453	7	US-10-085-783A-35025
5	327	100.0	467	7	US-10-242-535A-39933
6	327	100.0	467	7	US-10-085-783A-39933
7	327	100.0	471	7	US-10-242-535A-57254
8	327	100.0	471	7	US-10-085-783A-57254
9	327	100.0	472	7	US-10-242-535A-56068
10	327	100.0	472	7	US-10-085-783A-56068
11	327	100.0	508	8	US-10-913-937-3
12	327	100.0	523	7	US-10-242-535A-46292
13	325	99.4	476	3	US-09-918-995-17191
14	325	99.4	476	3	US-10-085-783A-46292
15	321	98.2	4543	5	US-10-198-846-11311
16	308	94.2	4476	8	US-10-357-930-25604
17	296	90.5	3484	8	US-10-723-860-1383
18	296	90.5	3484	9	US-10-756-149-1357
19	296	90.5	5111	5	US-10-205-823-382
20	296	90.5	5111	10	US-11-051-454-382
21	296	90.5	5371	8	US-10-723-860-5852
22	270	82.6	468	7	US-10-242-535A-47656
23	270	82.6	468	7	US-10-085-783A-47656

c	24	267	81.7	5347	6	US-10-240-965-99	Sequence 99, Appl
	25	249	76.1	3208	3	US-09-780-016-27	Sequence 27, Appl
	26	249	76.1	3208	5	US-10-214-811-27	Sequence 27, Appl
	27	249	76.1	3208	7	US-10-766-074-27	Sequence 27, Appl
	28	249	76.1	3208	10	US-11-036-185-27	Sequence 27, Appl
	29	209	63.9	509	9	US-10-450-763-22649	Sequence 22649, A
	30	207	63.3	430	7	US-10-242-535A-54751	Sequence 54751, A
	31	207	63.3	430	7	US-10-085-783A-54751	Sequence 54751, A
	32	198	60.6	475	7	US-10-242-535A-50604	Sequence 50604, A
	33	198	60.6	475	7	US-10-085-783A-50604	Sequence 50604, A
	34	173	52.9	300	7	US-10-242-535A-48516	Sequence 48516, A
	35	173	52.9	300	7	US-10-085-783A-48516	Sequence 48516, A
	36	170	52.0	439	3	US-09-918-995-14771	Sequence 14771, A
	37	166	50.8	380	3	US-09-960-352-4677	Sequence 4677, Ap
	38	163	49.8	370	7	US-10-242-535A-19847	Sequence 19847, A
	39	163	49.8	370	7	US-10-085-783A-19847	Sequence 19847, A
	40	157	48.0	318	7	US-10-242-535A-25733	Sequence 25733, A
	41	157	48.0	318	7	US-10-085-783A-25733	Sequence 25733, A
	42	149	45.6	666	9	US-10-450-763-22648	Sequence 22648, A
	43	148	45.3	486	7	US-10-242-535A-52747	Sequence 52747, A
	44	148	45.3	486	7	US-10-085-783A-52747	Sequence 52747, A
c	45	147	45.0	398	9	US-10-450-763-22645	Sequence 22645, A

ALIGNMENTS

RESULT 1
US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377
Query Match 100.0%; Score 327; DB 7; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGCGCGATGGATGGATATCCCGAGCGGCGACCAACAGCGCGCGGCGGCAAGAAG 60
Db 20 ATGGCGGCGCGATGGATGGATATCCCGAGCGGCGACCAACAGCGCGCGGCGGCAAGAAG 79
Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
Db 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 139
Qy 121 AACTGTGCCATCTGCAGGAACCAATATATGATGATCTTTGCATAGATGCTCAAGCTAACCG 180
Db 140 AACTGTGCCATCTGCAGGAACCAATATATGATGATCTTTGCATAGATGCTCAAGCTAACCG 199
Qy 181 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCCGATGGGAGTCTGTACCAATGCTTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCCGATGGGAGTCTGTACCAATGCTTTTTCAC 259

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 319
QY 301 TGGGAATTCCAAAGATATGGCACTAG 327
Db 320 TGGGAATTCCAAAGATATGGCACTAG 346

RESULT 2

US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-43377

Query Match 100.0%; Score 327; DB 7; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.8e-173; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;
QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 20 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTTGGTTGAT 120
Db 80 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTTGGTTGAT 139
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 180
Db 140 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 199
QY 181 GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 200 GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 319
QY 301 TGGGAATTCCAAAGATATGGCACTAG 327
Db 320 TGGGAATTCCAAAGATATGGCACTAG 346

RESULT 3

US-10-242-535A-35025
; Sequence 35025, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-35025

Query Match 100.0%; Score 327; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.8e-173; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;
QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 24 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 83
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTTGGTTGAT 120
Db 84 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTTGGTTGAT 143
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 180
Db 144 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 203
QY 181 GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 204 GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 263
QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 323
QY 301 TGGGAATTCCAAAGATATGGCACTAG 327
Db 324 TGGGAATTCCAAAGATATGGCACTAG 350

RESULT 4

US-10-085-783A-35025
; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

Query Match 100.0%; Score 327; DB 7; Length 453;


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; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57254
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Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 17 ATGGCGGCGAGCGATGGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
QY 61 CGCTTTGAAAGTGAAGATGGAATGCAATGCGATGCGATGCGGCTCTGGGCTGGGATATTGTTGTTGAT 120
DB 77 CGCTTTGAAAGTGAAGATGGAATGCAATGCGATGCGATGCGGCTCTGGGCTGGGATATTGTTGTTGAT 136
QY 121 AACTGTGCCATCTGCGAGGAACCAATATGGAATCTTTGATAGAAATGTCGAAGTAAACCAAG 180
DB 137 AACTGTGCCATCTGCGAGGAACCAATATGGAATCTTTGATAGAAATGTCGAAGTAAACCAAG 196
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGCGGAGTCTGTAAACCATGCTTTTCAC 240
DB 197 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGCGGAGTCTGTAAACCATGCTTTTCAC 256
QY 241 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACACACAGAGAG 300
DB 257 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACACACAGAGAG 316
QY 301 TGGGAATTCAGAAAGTATGGGCACTAG 327
DB 317 TGGGAATTCAGAAAGTATGGGCACTAG 343
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RESULT 8

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US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57254
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Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGGCGAGCGATGGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 17 ATGGCGGCGAGCGATGGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
QY 61 CGCTTTGAAAGTGAAGATGGAATGCAATGCGATGCGGCTCTGGGCTGGGATATTGTTGTTGAT 120
DB 77 CGCTTTGAAAGTGAAGATGGAATGCAATGCGATGCGGCTCTGGGCTGGGATATTGTTGTTGAT 136
QY 121 AACTGTGCCATCTGCGAGGAACCAATATGGAATCTTTGATAGAAATGTCGAAGTAAACCAAG 180
DB 137 AACTGTGCCATCTGCGAGGAACCAATATGGAATCTTTGATAGAAATGTCGAAGTAAACCAAG 196
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGCGGAGTCTGTAAACCATGCTTTTCAC 240
DB 197 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGCGGAGTCTGTAAACCATGCTTTTCAC 256
QY 241 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACACACAGAGAG 300
DB 257 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACACACAGAGAG 316
QY 301 TGGGAATTCAGAAAGTATGGGCACTAG 327
DB 317 TGGGAATTCAGAAAGTATGGGCACTAG 343
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RESULT 9

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US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56068
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Query Match      100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 20 ATGGCGGCGAGCGATGGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAAGTGAAGATGGAATGCAATGCGATGCGGCTCTGGGCTGGGATATTGTTGTTGAT 120
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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCGCAAGAAG 60
Db 19 ATGGCGGCGAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCCATCTGCAGGAAACCAACATTTATGGATCTTTTGCATAGAAATGTCAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAAACCAACATTTATGGATCTTTTGCATAGAAATGTCAGCTAACCCAG 198
QY 181 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 318
QY 301 TGGGAATTCCAAAGATATGGGCACTAG 327
Db 319 TGGGAATTCCAAAGATATGGGCACTAG 345

RESULT 14
US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-17191

Query Match      99.4%; Score 325; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-172;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGGCGAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCGCAAGAAGCG 62
Db 74 GCGCGGCGAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCGCAAGAAGCG 133
QY 63 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 122
Db 134 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 193
QY 123 CTGTGCCATCTGCAGGAAACCAACATTTATGGATCTTTTGCATAGAAATGTCAGCTAACCCAGGC 182
; SEQ ID NO 46292

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Db 194 CTGTGCCATCTGCAGGAACACATTATGGATCTTTGTCATAGAAATGTCAAGCTAACCCAGGC 253
QY 183 GTCGGCTACTTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACTT 242
Db 254 GTCGGCTACTTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACTT 313
QY 243 CCATCGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCCATTGGACAAACAGAGAGTG 302
Db 314 CCATCGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCCATTGGACAAACAGAGAGTG 373
QY 303 GGAATTCAAAAGTATGGGCACTAG 327
Db 374 GGAATTCAAAAGTATGGGCACTAG 398

RESULT 15

US-10-198-846-11311/c
; Sequence 11311, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11311
; LENGTH: 4543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-11311

Query Match 98.2%; Score 321; DB 5; Length 4543;
Best Local Similarity 100.0%; Pred. No. 4.3e-170;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
Db 1085 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 1026
QY 67 GAAGTGAAGAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATAACTGT 126
Db 1025 GAAGTGAAGAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATAACTGT 966
QY 127 GCCATCTGCAGGAACACACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACAGGCGTCC 186
Db 965 GCCATCTGCAGGAACACACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACAGGCGTCC 906
QY 187 GCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCACCTCCAC 246
Db 905 GCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCACCTCCAC 846
QY 247 TGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCCATTGGACAAACAGAGAGTGGGAA 306
Db 845 TGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCCATTGGACAAACAGAGAGTGGGAA 786
QY 307 TTCCAAAAGTATGGGCACTAG 327
Db 785 TTCCAAAAGTATGGGCACTAG 765

Search completed: March 8, 2006, 16:07:15
Job time : 538.691 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	327	100.0	482	3	US-09-513-999C-3894	Sequence 3894, Ap
2	327	100.0	507	3	US-09-949-016-4940	Sequence 4940, Ap
3	327	100.0	508	3	US-09-914-324A-3	Sequence 3, Appli
4	249	76.1	3208	3	US-09-780-016-27	Sequence 27, Appl
5	249	76.1	3208	3	US-10-214-811-27	Sequence 27, Appl
6	249	76.1	3208	3	US-10-766-074-27	Sequence 27, Appl
7	170	52.0	402	3	US-09-513-999C-10371	Sequence 10371, A
8	170	52.0	463	3	US-09-621-976-15180	Sequence 15180, A
9	89	27.2	25274	3	US-09-949-016-16682	Sequence 16682, A
10	50	15.3	504	3	US-09-914-324A-5	Sequence 5, Appli
11	36	11.1	601	3	US-09-949-016-174803	Sequence 174803, A
12	20	6.1	411	3	US-09-640-211A-1731	Sequence 1731, Ap
C 13	18	5.5	287	3	US-09-270-767-26361	Sequence 26361, A
C 14	18	5.5	902	3	US-09-270-767-10881	Sequence 10881, A
C 15	18	5.5	3183	2	US-08-939-218A-1	Sequence 1, Appli
C 16	18	5.5	3187	6	PCR-US95-06815-1	Sequence 1, Appli
C 17	18	5.5	3192	2	US-08-706-037-26	Sequence 26, Appl
C 18	18	5.5	3192	2	US-08-940-661A-1	Sequence 1, Appli
C 19	18	5.5	3192	2	US-09-083-485-1	Sequence 1, Appli
C 20	18	5.5	3192	2	US-09-005-397-26	Sequence 26, Appl
C 21	18	5.5	4118	2	US-08-113-125A-3	Sequence 3, Appli
C 22	18	5.5	63563	3	US-09-596-002-33	Sequence 33, Appl
C 23	18	5.5	113283	3	US-09-949-016-16976	Sequence 16976, A
C 24	18	5.5	113283	3	US-09-949-016-16977	Sequence 16977, A

; PRIOR APPLICATION NUMBER: US 60/181,294
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 3208
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-780-016-27

Query Match 76.1%; Score 249; DB 3; Length 3208;
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	79	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	138
Db	2776	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	2835
QY	139	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	198
Db	2836	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	2895
QY	199	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	258
Db	2896	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	2955
QY	259	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	318
Db	2956	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	3015
QY	319	GGGCACTAG 327	
Db	3016	GGGCACTAG 3024	

RESULT 5

US-10-214-811-27
 ; Sequence 27, Application US/10214811
 ; Patent No. 6743621
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6743621el Human Proteases and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/214,811
 ; PRIOR FILING DATE: 2002-08-07
 ; PRIOR APPLICATION NUMBER: US/09/780,016
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,294
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 3208
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-214-811-27

Query Match 76.1%; Score 249; DB 3; Length 3208;
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	79	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	138
Db	2776	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	2835
QY	139	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	198

Db	2836	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	2895
QY	199	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	258
Db	2896	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	2955
QY	259	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	318
Db	2956	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	3015
QY	319	GGGCACTAG 327	
Db	3016	GGGCACTAG 3024	

RESULT 6

US-10-766-074-27
 ; Sequence 27, Application US/10766074
 ; Patent No. 6881563
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6881563el Human Proteases and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/766,074
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/10/214,811
 ; PRIOR FILING DATE: 2002-08-07
 ; PRIOR APPLICATION NUMBER: US/09/780,016
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,294
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 3208
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-766-074-27

Query Match 76.1%; Score 249; DB 3; Length 3208;
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	79	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	138
Db	2776	TGGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTCTGCACTCTGCAGG	2835
QY	139	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	198
Db	2836	AACCACATTATGGATCTTTGCATAGAAATGTCAGCTAACGAGGCGTCCGCTACTTCAGAA	2895
QY	199	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	258
Db	2896	GAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACTGCATCTCTCGC	2955
QY	259	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	318
Db	2956	TGGCTCAAAACACGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT	3015
QY	319	GGGCACTAG 327	
Db	3016	GGGCACTAG 3024	

RESULT 7

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US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10371
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Query Match          52.0%; Score 170; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.8e-82;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 GCATAGAATGCTCAAGCTAACCGAGTCCGCTACTTTCAGAAAGAGTGCTACTGTGCGCATGGG 217
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|
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Db 106 GCATAGAATGCTCAAGCTAACCGAGTCCGCTACTTTCAGAAAGAGTGCTACTGTGCGCATGGG 165
|
|
|
QY 218 GAGTCTGTAAACATGCTTTTTCATCTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGG 277
|
|
|
Db 166 GAGTCTGTAAACATGCTTTTTCATCTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGG 225
|
|
|
QY 278 TGTGTCCATTGGACAACAGAGTGGGAATTCAAAAGATATGGCACTAG 327
|
|
|
Db 226 TGTGTCCATTGGACAACAGAGTGGGAATTCAAAAGATATGGCACTAG 275
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|
|
RESULT 8
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
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US-09-621-976-15180

Query Match          52.0%; Score 170; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.9e-82;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 GCATAGAATGCTCAAGCTAACCGAGTCCGCTACTTTCAGAAAGAGTGCTACTGTGCGCATGGG 217
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|
|
Db 101 GCATAGAATGCTCAAGCTAACCGAGTCCGCTACTTTCAGAAAGAGTGCTACTGTGCGCATGGG 160
|
|
|
QY 218 GAGTCTGTAAACATGCTTTTTCATCTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGG 277
|
|
|
Db 161 GAGTCTGTAAACATGCTTTTTCATCTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGG 220
|
|
|
QY 278 TGTGTCCATTGGACAACAGAGTGGGAATTCAAAAGATATGGCACTAG 327
|
|
|
Db 221 TGTGTCCATTGGACAACAGAGTGGGAATTCAAAAGATATGGCACTAG 270
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|
|
RESULT 9
US-09-949-016-16682
; Sequence 16682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

Query Match          27.2%; Score 89; DB 3; Length 25274;
Best Local Similarity 100.0%; Pred. No. 5.4e-38;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 CATGCTTTTCACCTTCCACTGCACTCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTG 288
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|
|
Db 18411 CATGCTTTTCACCTTCCACTGCACTCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTG 18470
|
|
|
QY 289 GACAACAGAGAGTGGGAATTCAAAAGATA 317
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|
|
Db 18471 GACAACAGAGAGTGGGAATTCAAAAGATA 18499
|
|
|
RESULT 10
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-0046000S
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
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; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Query Match 15.3%; Score 50; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 6.1e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ATTGTGGTGTGATCTGTCATCTGCAGGAACCACTATGATCTTTG 158
Db 126 ATTGTGGTGTGATCTGTCATCTGCAGGAACCACTATGATCTTTG 175

RESULT 11

US-09-949-016-174803
; Sequence 174803, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174803
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-174803

Query Match 11.0%; Score 36; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGATGTCAGCTAACGAGCGGTCGCTACTT 193
Db 566 GCATAGATGTCAGCTAACGAGCGGTCGCTACTT 601

RESULT 12

US-09-640-211A-1731
; Sequence 1731, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(411)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1731

Query Match 6.1%; Score 20; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 TGGGATATTGTGGTTGATAA 122
Db 206 TGGGATATTGTGGTTGATAA 225

RESULT 13

US-09-270-767-26361/c
; Sequence 26361, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26361
; LENGTH: 287
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-26361

Query Match 5.5%; Score 18; DB 3; Length 287;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 AGTGGGAATTCCTCAAAAGT 316
Db 113 AGTGGGAATTCCTCAAAAGT 96

RESULT 14

US-09-270-767-10881/c
; Sequence 10881, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10881
; LENGTH: 902
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-10881

Query Match 5.5%; Score 18; DB 3; Length 902;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 AGTGGGAATTCCTCAAAAGT 316

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Db      728 AGTGGGAATTCCAAAAGT 711
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RESULT 15
US-08-939-218A-1/c
; Sequence 1, Application US/08939218A
; Patent No. 5981243
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy Michael
; APPLICANT: BROWN, Stephen H.
; APPLICANT: XU, Feng
; APPLICANT: SCHNEIDER, Pallo
; APPLICANT: OXENB LL, Karen M.
; APPLICANT: AASLYNG, Dorrit A.
; TITLE OF INVENTION: PURIFIED MYCELIOPTHORA LACCASES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5981243o No. 5981243disk of No. 5981243th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,218A
; FILING DATE: 29-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol E.
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4184.120-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(586..831, 917..994, 1079..1090, 1193..1264,
; LOCATION: 1337..2308, 2456..2524, 2618..3028)
US-08-939-218A-1

Query Match      5.5%; Score 18; DB 2; Length 3183;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      198 AGAGTGACTGTGCGCATG 215
Db      924 AGAGTGACTGTGCGCATG 907
|||||

Search completed: March 8, 2006, 14:34:35
Job time : 114.91 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 10:15:10 ; Search time 3736 Seconds
(without alignments)
4095.122 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgacgcatgatgt.....tccaaagatgggactag 327

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 12

Total number of hits satisfying chosen parameters: 897482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	462	7	CN305890 170005830
2	327	100.0	471	2	BG339057 602436882
3	327	100.0	473	5	BX283972 BX283972
4	327	100.0	488	2	BG777485 602664820
5	327	100.0	498	6	CB296618 12822006
6	327	100.0	509	7	CN305892 170006001
7	327	100.0	518	3	BP420485 BP420485
8	327	100.0	522	1	AL711573 DKFZp6861
9	327	100.0	525	2	BG337472 602435003
10	327	100.0	527	3	BW715215 UI-E-CL1-
11	327	100.0	527	5	BW715215 UI-E-CL1-
12	327	100.0	527	6	CB999822 AGENCOURT
13	327	100.0	529	3	BW757406 K-EST0036
14	327	100.0	531	6	CD523457 AGENCOURT
15	327	100.0	533	5	BW729963 UI-E-CK1-
16	327	100.0	537	2	BG478622 602525509
17	327	100.0	545	5	BW941262 AGENCOURT
18	327	100.0	546	2	B1198015 602762132
19	327	100.0	546	5	BW601181 AGENCOURT
20	327	100.0	548	1	AV716338 AV716338
21	327	100.0	548	5	BW601301 AGENCOURT
22	327	100.0	549	3	BI858425 603386437

23	327	100.0	550	5	BU955646
24	327	100.0	554	6	CD249363
25	327	100.0	555	5	BU532840
26	327	100.0	555	5	BU601080
27	327	100.0	557	5	BU954591
28	327	100.0	558	6	CD388268
29	327	100.0	559	7	CK003869
30	327	100.0	562	6	CD175085
31	327	100.0	563	5	BU861191
32	327	100.0	570	5	BU597842
33	327	100.0	573	5	BU533405
34	327	100.0	581	3	BP308845
35	327	100.0	583	3	BP317451
36	327	100.0	616	2	BG705958
37	327	100.0	736	2	BG503311
38	327	100.0	801	5	BU533420
39	327	100.0	845	5	BU959349
40	327	100.0	886	2	BG481544
41	327	100.0	904	3	BM459634
42	327	100.0	945	3	BQ216738
43	327	100.0	1098	3	BQ050461
44	326	99.7	403	2	BG531117
45	326	99.7	448	2	BE738587

ALIGNMENTS

RESULT 1
CN305890 170005830 462 bp mRNA linear EST 16-MAY-2004
LOCUS GRN_PRESHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN305890
VERSION CN305890.1 GI:47322304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (Bases 1 to 462)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Gen Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@gen.com
Insert Length: 462 Std Error: 0.00.
FEATURES
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1..462
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PRESHEP"
/notes="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Query Match 100.0%; Score 327; DB 7; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 23 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 82
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CGCTTTGAAGTGAAGAAAGTGAAGTGCAGTACGCCCTCTGGGCCTGGGATATTGGTTGAT 120
Db CGCTTTGAAGTGAAGAAAGTGAAGTGCAGTACGCCCTCTGGGCCTGGGATATTGGTTGAT 142
QY 121 AACTGTGCCATCTGCAGGAACCAACATATTGATCTTTGCATAGATAATGCTCAAGCTAACAG 180
Db AACTGTGCCATCTGCAGGAACCAACATATTGATCTTTGCATAGATAATGCTCAAGCTAACAG 202
QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 262
QY 241 TTCCACTTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTGGACAAACAGAGAG 300
Db TTCCACTTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTGGACAAACAGAGAG 322
QY 301 TGGGAATTCACAAAGTATGGCACTAG 327
Db TGGGAATTCACAAAGTATGGCACTAG 349

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RESULT 2
BG339057 602436882F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554597 5',
LOCUS mRNA sequence.
DEFINITION BG339057.1 GI:13145495
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-roman@nsl.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1254 row: d column: 22
High quality sequence stop: 470.

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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4554597"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

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Query Match 100.0%; Score 327; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 42 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 101
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CGCTTTGAAGTGAAGAAAGTGAAGTGCAGTACGCCCTCTGGGCCTGGGATATTGGTTGAT 120
Db CGCTTTGAAGTGAAGAAAGTGAAGTGCAGTACGCCCTCTGGGCCTGGGATATTGGTTGAT 161
QY 121 AACTGTGCCATCTGCAGGAACCAACATATTGATCTTTGCATAGATAATGCTCAAGCTAACAG 180
Db AACTGTGCCATCTGCAGGAACCAACATATTGATCTTTGCATAGATAATGCTCAAGCTAACAG 221
QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 281
QY 241 TTCCACTTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTGGACAAACAGAGAG 300
Db TTCCACTTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTGGACAAACAGAGAG 341
QY 301 TGGGAATTCACAAAGTATGGCACTAG 327
Db TGGGAATTCACAAAGTATGGCACTAG 368

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RESULT 3
BX283972 473 bp mRNA linear EST 05-MAR-2003
LOCUS BX283972 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:958P131435 ;
DEFINITION IMAGE:4652028, mRNA sequence.
ACCESSION BX283972
VERSION BX283972.1 GI:28848426
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

```

REFERENCE 1 (bases 1 to 473)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp958P131435.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

```

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This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
pCMV-M13u, Primer sequence: CGTTGTAACAGCAGCCGCACT.
FEATURES
source
1..473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:958P131435 ; IMAGE:4652028"
/tissue_type="choriocarcinoma"
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FEATURES	Location/Qualifiers	
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	/clone="12B22006_rev_1_C10_r_082.ab1"	
	/sex="male"	
	/tissue_type="brain, presumably cortex"	
	/dev_stage="adult"	
	/lab_host="Epicurian Coli (TM) XL-10-Gold"	
	/clone_lib="Chimpanzee brain library Koo"	
	/note="Vector: pUCH1; Site 1: SfiI-A; Site 2: SfiI-B; The library was prepared using the SMART cDNA library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid Vector."	
	ORIGIN	
	Query Match 100.0%; Score 327; DB 6; Length 498;	
	Best Local Similarity 100.0%; Pred. No. 6.6e-175;	
	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGGCAAG 60
DB	2	ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGGCAAG 61
QY	61	CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTTGAT 120
DB	62	CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTTGAT 121
QY	121	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGATGCTCAAGCTAAC 180
DB	122	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGATGCTCAAGCTAAC 181
QY	181	GCCTCCGCTACTTCAGAAGAGTGTCTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB	182	GCCTCCGCTACTTCAGAAGAGTGTCTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 241
QY	241	TTCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 300
DB	242	TTCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 301
QY	301	TGGGAATTCAAAAGTATGGGCACCTAG 327
DB	302	TGGGAATTCAAAAGTATGGGCACCTAG 328
RESULT 6		
CN305892		
LOCUS 509 bp mRNA linear EST 16-MAY-2004		
DEFINITION 1700600185586 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.		
ACCESSION CN305892		
VERSION CN305892.1 GI:47322306		
KEYWORDS EST.		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 509)		
AUTHORS Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.		
TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation		
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)		
PUBMED 15146197		
COMMENT Contact: Brandenberger R		
Regenerative Medicine		
Geron Corporation		
230 Constitution Drive, Menlo Park, CA 94025, USA		
Tel: 650 473 8658		
Fax: 650 473 7760		
Email: rbrandenberger@geron.com		
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Location/Qualifiers		
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/clone_lib="GRN_PRENEU"		
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."		
ORIGIN		
Query Match 100.0%; Score 327; DB 7; Length 509;		
Best Local Similarity 100.0%; Pred. No. 6.6e-175;		
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGGCAAG 60
DB	6	ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGGCAAG 65
QY	61	CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTTGAT 120
DB	66	CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTTGAT 125
QY	121	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGATGCTCAAGCTAAC 180
DB	126	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGATGCTCAAGCTAAC 185
QY	181	GCCTCCGCTACTTCAGAAGAGTGTCTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB	186	GCCTCCGCTACTTCAGAAGAGTGTCTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 245
QY	241	TTCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 300
DB	246	TTCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 305
QY	301	TGGGAATTCAAAAGTATGGGCACCTAG 327
DB	306	TGGGAATTCAAAAGTATGGGCACCTAG 332
RESULT 7		
BP420485		
LOCUS 518 bp mRNA linear EST 27-MAY-2005		
DEFINITION BP420485 Homo sapiens small intestine Homo sapiens cDNA clone HIE03775r 3', mRNA sequence.		
ACCESSION BP420485		
VERSION BP420485.1 GI:66786738		
KEYWORDS EST.		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 518)		
AUTHORS Takeda, J., Jin, L. and Horikawa, Y.		
TITLE Expression profile of mRNAs from human pancreatic islet tumors		
JOURNAL Unpublished (2005)		
COMMENT Contact: Yukio Horikawa		
Laboratory of Molecular Genetics		
Institute for Molecular and Cellular Regulation, Gunma University		
Shima-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan		
Tel: 81-27-220-8832		
Fax: 81-27-220-8889		
Email: yhorikawa@showa.gunma-u.ac.jp.		
Location/Qualifiers		
1. .518		
/organism="Homo sapiens"		

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/clone="HIE03775r"  
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ORIGIN

Query Match	100.0%	Score 327;	DB 3;	Length 518;
Best Local Similarity	100.0%	Pred. No. 6.6e-175;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCGCAGCGATGGATGTGGATATCCCGAGCGGCCAACACAGCGCGCGGCAAGAAG	60	
Db	14	ATGCGCAGCGATGGATGTGGATATCCCGAGCGGCCAACACAGCGCGCGGCAAGAAG	73	
QY	61	CGCTTTCAAGTGAAAAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT	120	
Db	74	CGCTTTCAAGTGAAAAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT	133	
QY	121	AACGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG	180	
Db	134	AACGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG	193	
QY	181	GCGTCCGCTACTTCAGAAGAGTGACTGTCGCATGGGAGTCTGTGAACCATGCTTTTCAC	240	
Db	194	GCGTCCGCTACTTCAGAAGAGTGACTGTCGCATGGGAGTCTGTGAACCATGCTTTTCAC	253	
QY	241	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAAACAGAGAG	300	
Db	254	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAAACAGAGAG	313	
QY	301	TGGGAATTCAAAAGTATGGGCACCTAG	327	
Db	314	TGGGAATTCAAAAGTATGGGCACCTAG	340	

RESULT	8
LOCUS	AL7111573
DEFINITION	DKFZP686I0483_r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION	AF292686I0483 5', mRNA sequence.
VERSION	AL7111573
KEYWORDS	AL7111573.1 GI:19694928
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 522)
AUTHORS	Koehler,K., Beyer,A., Mewes,W., Weill,B. and Wiemann,S.
TITLE	EST (Koehler,K., Beyer,A., Mewes,H.W., Weill,B. and Wiemann,S.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS

FEATURES
source

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/issue type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:4553064"

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ORIGIN

Query Match	100.0.0%;	Score 327;	DB 1;	Length 522;
Best Local Similarity	100.0.0%;	Pred. No. 6.6e-175;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGCGCACCAACAGCGCGCGCGGCAAGAAG	60	
DB	21	ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGCGCACCAACAGCGCGCGCGGCAAGAAG	80	
QY	61	CGCTTTTGAAGTGAATAAGTGGATGCAAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	120	
DB	81	CGCTTTTGAAGTGAATAAGTGGATGCAAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	140	
QY	121	AACGTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAAATGTCACAGCTAACCAAG	180	
DB	141	AACGTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAAATGTCACAGCTAACCAAG	200	
QY	181	GCCTTCGCTACTTTCAGAAAGTAGTACTGTGCGCATGGGGAGTCTCTGAACCATGCTTTTTCAC	240	
DB	201	GCCTTCGCTACTTTCAGAAAGTAGTACTGTGCGCATGGGGAGTCTCTGAACCATGCTTTTTCAC	260	
QY	241	TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG	300	
DB	261	TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG	320	
QY	301	TGGGAATTCCAAAGTAGTGGGCACCTAG	327	
DB	321	TGGGAATTCCAAAGTAGTGGGCACCTAG	347	

RESULT 9

[illegible]

FEATURES
SOURCE

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1. 323
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4553064"
/tissue_type="leiomyosarcoma"
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/clone_lib="NIH_MGC_46"
note=organ: uterus; Vector:

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RESULT 13
BM757406
LOCUS
DEFINITION
    BM757406 529 bp mRNA linear EST 04-MAR-2002
    K-EST0036388 SISNU5 Homo sapiens cDNA clone S1SNUS-29-H12 5', mRNA
    sequence.
ACCESSION
BM757406
VERSION
BM757406.1 GI:19087021
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 529)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
UNPUBLISHED (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 ROW: H column: 12
High quality sequence stop: 529.
Location/Qualifiers
    1..529
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="S1SNUS-29-H12"
        /sex="F"
        /tissue_type="Ascites"
        /cell_type="Lymphoblast-like"
        /lab_host="SNU-5"
        /lab_host="Top10P"
        /clone_lib="S1SNUS"
        /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
        Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
        bacterial alkaline phosphatase (BAP) and then decapped
        with Tabacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including EcoR
        I site by treatment of T4 RNA ligase and the first strand
        cDNA was synthesized from oligo dt-selected mRNA by
        priming with dt-tailed vector. The dt-tailed vector was
        adjusted to have about 60nt. The cDNA vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10P by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."
FEATURES
    source
        1..529
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="S1SNUS-29-H12"
            /sex="F"
            /tissue_type="Ascites"
            /cell_type="Lymphoblast-like"
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            /lab_host="Top10P"
            /clone_lib="S1SNUS"
            /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
            Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then decapped
            with Tabacco acid pyrophosphatase (TAP). The decapped
            intact mRNA was ligated with DNA-RNA linker including EcoR
            I site by treatment of T4 RNA ligase and the first strand
            cDNA was synthesized from oligo dt-selected mRNA by
            priming with dt-tailed vector. The dt-tailed vector was
            adjusted to have about 60nt. The cDNA vector was
            circularized with E. coli DNA ligase after digestion of
            EcoRI which site is also included in vector. An RNA strand
            converted to a DNA strand by Okayama-Berg method. The
            obtained cDNA vectors were used for transformation of
            competent cells E. coli Top10P by electroporation method.
            The cDNA libraries constructed by this method are
            full-length enriched cDNA library."
ORIGIN
Query Match 100.0%; Score 327; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGGATGGATGGATATCCCGAGCGGCCACACACGGCGGGGCAAGAAG 60
DB 1 |
DB 33 ATGGCGGCGGATGGATGGATATCCCGAGCGGCCACACACGGCGGGGCAAGAAG 92
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 93 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 152
QY 121 AACTGTGCCATCTCGAGGAACACATATGATGATCTTTGCATAGATGTCAGCTAACACAG 180

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DB 153 AACTGTGCCATCTCGAGGAACACATATGATGATCTTTGCATAGATGTCAGCTAACACAG 212
QY 181 GGTGCGGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTTCAC 240
DB 213 GGTGCGGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTTCAC 272
QY 241 TTCCACTGTCATCTCGCTGGCTCAAAACACACACAGGAGTGTGTCATTGGACAAACAGAGAG 300
DB 273 TTCCACTGTCATCTCGCTGGCTCAAAACACACAGGAGTGTGTCATTGGACAAACAGAGAG 332
QY 301 TGGGAATTCCTCAAAAGTATGGCACTAG 327
DB 333 TGGGAATTCCTCAAAAGTATGGCACTAG 359

CD523457 531 bp mRNA linear EST 06-JUN-2003
AGENCOURT 14360071 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30412182 5', mRNA sequence.
CD523457
CD523457
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 531)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Daniela S. Gerhard, Ph.D.
COMMENT
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDCM205 row: c column: 07
High quality sequence stop: 518.
Location/Qualifiers
    1..531
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:30412182"
        /tissue_type="Pooled"
        /lab_host="DH10B (TI phase-resistant)"
        /clone_lib="NIH_MGC_191"
        /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
        Site_2: SfiI (ggcgctctggcc); Library is oligo-dT primed
        and directionally cloned. PBMC - Peripheral Blood
        Mononuclear Cells. RNA was pooled from 3/6hour stimulation
        with PMA adn Ionomycin. 5' and 3' adaptors were used in
        cloning as follows: 5' adaptor sequence:
        5'-CACGGCCATTATGGCC-3, and 3' adaptor sequence:
        5'-ATTCTAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,
        C, G and N = A, C, G, or T). Average insert size 1.69
        kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
        by PCR. This library was enriched for full-length clones
        and was constructed by Clontech Laboratories (Palo Alto,
        CA). Note: this is a NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 327; DB 6; Length 531;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;

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Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATATACCCCGAGCGGACCAACAGCGGCGGCGGAAG 60
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 Db 23 ATGGCGGAGGATGGATGGATATACCCCGAGCGGACCAACAGCGGCGGCGGAAG 82
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 Qy 61 CGCTTTGAAGTGAAAAGTGAATGAGTACGCTCTGGGCTCTGGGATATTTGGTTGAT 120
 |||||
 Db 83 CGCTTTGAAGTGAAAAGTGAATGAGTACGCTCTGGGCTCTGGGATATTTGGTTGAT 142
 |||||
 Qy 121 AACTGTGTCATCTGCAGCAACACATTTGATCTTTCATAGATGTCAGCTAACCCAG 180
 |||||
 Db 143 AACTGTGTCATCTGCAGCAACACATTTGATCTTTCATAGATGTCAGCTAACCCAG 202
 |||||
 Qy 181 CGCTCCGCTACTTCAGAGAGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 240
 |||||
 Db 203 CGCTCCGCTACTTCAGAGAGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 262
 |||||
 Qy 241 TTCACATGCTCTCTCGCTGCTGCTCAAAACAGCAGGAGTGTCTCAATTGGACAAACAGAG 300
 |||||
 Db 263 TTCACATGCTCTCTCGCTGCTGCTCAAAACAGCAGGAGTGTCTCAATTGGACAAACAGAG 322
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 Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
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 Db 323 TGGGAATTCCAAAGTATGGCACTAG 349
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RESULT 15

BU729963/c

LOCUS BU729963 533 bp mRNA linear EST 09-OCT-2002

DEFINITION UI-E-CK1-afi-h-19-0-UI.s1 UI-E-CK1 Homo sapiens cDNA clone

ACCESSION BU729963

VERSION UI-E-CK1-afi-h-19-0-UI 3', mRNA sequence.

KEYWORDS BU729963.1 GI:23653376

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 533)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..533

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afi-h-19-0-UI"

/issue_type="Retina Foveal and Macular"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-CK1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG TISSUE=Foveal and Macular Retina

TAG_LIB=UI-E-CK1

TAG_SEQ=GTCC"

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 533;
 Best Local Similarity. 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATATACCCCGAGCGGACCAACAGCGGCGGCGGAAG 60
 |||||
 Db 518 ATGGCGGAGGATGGATGGATATACCCCGAGCGGACCAACAGCGGCGGCGGAAG 459
 |||||
 Qy 61 CGCTTTGAAGTGAAAAGTGAATGAGTACGCTCTGGGCTCTGGGATATTTGGTTGAT 120
 |||||
 Db 458 CGCTTTGAAGTGAAAAGTGAATGAGTACGCTCTGGGCTCTGGGATATTTGGTTGAT 399
 |||||
 Qy 121 AACTGTGCTCATCTGCAGAAACCAACATTTGATCTTTGTCATAGATGTCAGCTAACCCAG 180
 |||||
 Db 398 AACTGTGCTCATCTGCAGAAACCAACATTTGATCTTTGTCATAGATGTCAGCTAACCCAG 339
 |||||
 Qy 181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 240
 |||||
 Db 338 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 279
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 Qy 241 TTCACATGCTCTCTCGCTGCTGCTCAAAACAGCAGGAGTGTCTCAATTGGACAAACAGAG 300
 |||||
 Db 278 TTCACATGCTCTCTCGCTGCTGCTCAAAACAGCAGGAGTGTCTCAATTGGACAAACAGAG 219
 |||||
 Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
 |||||
 Db 218 TGGGAATTCCAAAGTATGGCACTAG 192
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RESULT 16

BU729963

LOCUS BU729963 537 bp mRNA linear EST 21-MAR-2001

DEFINITION 602525509F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643619 5', mRNA sequence.

ACCESSION BU729963

VERSION BU729963.1 GI:13410901

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-i@mail.nih.gov

Tissue Procurement: ATCC/DCTB/DTp

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 546)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1001786 row: 0 column: 07
High quality sequence stop: 525.

FEATURES

source

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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4897758"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGACCAACAGCGGCGGGAAGAAG 60
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Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 78 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 137
Qy 121 AACTGTGCGCATCTCGAGGAACACATATATGATCTTTGCATAGATGTCAAGCTAACAG 180
Db 138 AACTGTGCGCATCTCGAGGAACACATATATGATCTTTGCATAGATGTCAAGCTAACAG 197
Qy 181 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTTCAC 240
Db 198 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTTCAC 257
Qy 241 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGGAGTGTCTTCCATTGGACACAGAG 300
Db 258 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGGAGTGTCTTCCATTGGACACAGAG 317
Qy 301 TGGGAATTCACAAAGATGGGCACTAG 327
Db 318 TGGGAATTCACAAAGATGGGCACTAG 344

RESULT 19
BU601181 546 bp mRNA linear EST 20-SEP-2002
LOCUS AGENCOURT 10029786 NIH_MGC_142 Homo sapiens cDNA clone
DEFINITION IMAGE:6495061 5', mRNA sequence.
ACCESSION BU601181
VERSION BU601181.1 GI:23252940
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 546)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1001786 row: 0 column: 14
High quality sequence stop: 491.

FEATURES

source

1..546
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6495061"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_142"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGGTATCAACGAGTGGCCATTACGGCGG-3' and
5'-ATTCTAGAGCGGCGGCGGAGATG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 546;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGACCAACAGCGGCGGGAAGAAG 60
Db 13 ATGGCGGAGGATGGATGGATACCCCGAGCGGACCAACAGCGGCGGGAAGAAG 72
Qy 61 CGCTTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 73 CGCTTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 132
Qy 121 AACTGTGCGCATCTCGAGGAACACATATATGATCTTTGCATAGATGTCAAGCTAACAG 180
Db 133 AACTGTGCGCATCTCGAGGAACACATATATGATCTTTGCATAGATGTCAAGCTAACAG 192
Qy 181 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTTCAC 240
Db 193 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTTCAC 252
Qy 241 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGGAGTGTCTTCCATTGGACACAGAG 300
Db 253 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGGAGTGTCTTCCATTGGACACAGAG 312
Qy 301 TGGGAATTCACAAAGATGGGCACTAG 327

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGACCAACAGAGAG 300
 Db 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGACCAACAGAGAG 316
 QY 301 TGGGAATTCCTCAAAAGATATGGCACTAG 327
 Db 317 TGGGAATTCCTCAAAAGATATGGCACTAG 343

RESULT 22
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 DEFINITION 603386437F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5395281 5', mRNA sequence.
 ACCESSION BI858425
 VERSION BI858425.1 GI:15999172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloning distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM12007 row: i column: 10
 High quality sequence stop: 525.
 FEATURES
 Location/Qualifiers
 1..549
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5395281"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_87"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 3; Length 549;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCGCGCAGCATGTGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
 Db 1 ATGCGCGCAGCATGTGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
 QY 61 CGCTTTCAAGTGAAGATGCAGTAGCCTCTGGCCCTGGGATATTTGGTTGAT 120
 Db 61 CGCTTTCAAGTGAAGATGCAGTAGCCTCTGGCCCTGGGATATTTGGTTGAT 120
 QY 121 AACTGTGCCATCTCAGCAACCAATATGATCTTTGCATAGATGCTCAAGCTAACCAAG 180
 Db 121 AACTGTGCCATCTCAGCAACCAATATGATCTTTGCATAGATGCTCAAGCTAACCAAG 180
 QY 181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTAC 240
 Db 181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTAC 240

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGACCAACAGAGAG 300
 Db 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGACCAACAGAGAG 300
 QY 301 TGGGAATTCCTCAAAAGATATGGCACTAG 327
 Db 301 TGGGAATTCCTCAAAAGATATGGCACTAG 327

RESULT 23
 LOCUS BU955646 550 bp mRNA linear EST 21-OCT-2002
 DEFINITION AGENCOURT 10612538 NIH_MGC 126 Homo sapiens cDNA clone IMAGE:6727878 5', mRNA sequence.
 ACCESSION BU955646
 VERSION BU955646.1 GI:24185218
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 550)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloning distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLCM3048 row: j column: 05
 High quality sequence stop: 520.
 FEATURES
 Location/Qualifiers
 1..550
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6727878"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC 126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctcggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAGCAGATGGCATTCAGCGCGG-3' and
 5'-ATTCTAGAGCCGAGCGCGGCGGACATG-dr(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC 127 and NIH_MGC 128). Library created in the laboratory of T. Uesdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 5; Length 550;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCGCGCAGCATGTGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
 Db 17 ATGCGCGCAGCATGTGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76

FEATURES
source
 Location/Qualifiers
 1. .557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6726227"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGAGATGGCCATTACGCCGGG-3' and 5'-ATTCTAGAGCGGCGGCGGCGGATG-30NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 5; Length 557;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGGCGGCGCAAGAAG 60
 DB 22 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGGCGGCGCAAGAAG 81
 QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
 DB 82 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 141
 QY 121 AACTGTGCCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAGCTTAACCA 180
 DB 142 AACTGTGCCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAGCTTAACCA 201
 QY 181 GCGTCGCGTACTTCAGAGAGTGTACTGCGATCGGAGTCTGTAACCATGCTTTTCAC 240
 DB 202 GCGTCGCGTACTTCAGAGAGTGTACTGCGATCGGAGTCTGTAACCATGCTTTTCAC 261
 QY 241 TTCCACTGTCATCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACACAGAGAG 300
 DB 262 TTCCACTGTCATCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACACAGAGAG 321
 QY 301 TGGGAATTCCTCAAGATGATGGCACTAG 327
 DB 322 TGGGAATTCCTCAAGATGATGGCACTAG 348

RESULT 28
 CD388268
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 558)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

FEATURES
source
 Location/Qualifiers
 1. .557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6726227"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGAGATGGCCATTACGCCGGG-3' and 5'-ATTCTAGAGCGGCGGCGGCGGATG-30NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 6; Length 558;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGGCGGCGCAAGAAG 60
 DB 32 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGGCGGCGCAAGAAG 91
 QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
 DB 92 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 151
 QY 121 AACTGTGCCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAGCTTAACCA 180
 DB 152 AACTGTGCCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAGCTTAACCA 211
 QY 181 GCGTCGCGTACTTCAGAGAGTGTACTGCGATCGGAGTCTGTAACCATGCTTTTCAC 240
 DB 212 GCGTCGCGTACTTCAGAGAGTGTACTGCGATCGGAGTCTGTAACCATGCTTTTCAC 271
 QY 241 TTCCACTGTCATCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACACAGAGAG 300
 DB 272 TTCCACTGTCATCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACACAGAGAG 331
 QY 301 TGGGAATTCCTCAAGATGATGGCACTAG 327
 DB 332 TGGGAATTCCTCAAGATGATGGCACTAG 358

RESULT 29
 CD388268
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 559)
 NIH-MGC http://mgi.nci.nih.gov/

COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDR80 row: h column: 04
 High quality sequence start: 13
 High quality sequence stop: 558.
 Location/Qualifiers
 1. .558
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic trophoblasts, made from WA01 stem cells"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_173"
 /note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
 LIBR PRIMING - oligo dt; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: gcapbs@email.nih.gov Tissue Procurement: Professor Miklss Palkovits cDNA Library Preparation: Michael Brownstein / Ted Usdin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDCM264 row: n column: 01 High quality sequence stop: 543.		
FEATURES	Location/Qualifiers		
source	1. 559 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30719640" /tissue_type="Human Brain - Cerebellar Cortex" /lab_host="DH10B Tona" /clone_lib="NIH_MGC_228" /notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: Sfil (directional); Site 2: Sfil (directional); Library is oligo-dT primed and directionally cloned.5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGGTGATCAACGACAGTGGCCATTACGCGGG-3'5'-ATTCTAGAGG CCAGCGCGGCATG-d(T)3N-IN-3. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected for >0.5kb with an average insert size of 1.2kb Library created in the laboratory of Jonathan Kuo and Ted Usdin."		
ORIGIN	Query Match 100.0%; Score 327; DB 7; Length 559; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGCGGCACGGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGCGGCAGAGAAG	60
Db	23	ATGCGGCACGGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGCGGCAGAGAAG	82
QY	61	CGCTTTGAAGTGAAGAAGTGGATGCAATGAGTCCCTCTGGCGCTGGGATATGTGGTTGAT	120
Db	83	CGCTTTGAAGTGAAGAAGTGGATGCAATGAGTCCCTCTGGCGCTGGGATATGTGGTTGAT	142
QY	121	AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCAATAGATGTCAAGCTCAACCAAG	180
Db	143	AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCAATAGATGTCAAGCTCAACCAAG	202
QY	181	GCCTCCGCTACTTCAGAAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC	240
Db	203	GCCTCCGCTACTTCAGAAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC	262
QY	241	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTGGACACACAGAG	300
Db	263	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCATTGGACACACAGAG	322
QY	301	TGGGAATTCCAAAAGATGGGCACTAG	327
Db	323	TGGGAATTCCAAAAGATGGGCACTAG	349
RESULT 30			
CD175085			
LOCUS	CD175085	562 bp	mRNA linear EST 19-MAY-2003
DEFINITION	AGENCOURT_13976103 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.		
ACCESSION	CD175085		
VERSION	CD175085.1 GI:30859303		

[illegible]

QY 181 GCGTCGGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATCTTTTAC 240
 |||||
 Db 212 GCGTCGGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATCTTTTAC 271
 |||||
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGCCATTGGACAACAGAG 300
 |||||
 Db 272 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGCCATTGGACAACAGAG 331
 |||||
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 |||||
 Db 332 TGGGAATTCAAAAGTATGGGCACTAG 358
 |||||

RESULT 33
 BU533405
 LOCUS BU533405 573 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT.10197895 NIH_MGC_126 Homo sapiens cDNA clone
 IMAGE:6559746 5', mRNA sequence.

ACCESSION BU533405
 VERSION BU533405.1 GI:22843846
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

REFERENCE 1 (bases 1 to 573)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Cloned Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM2731 row: h column: 18
 High quality sequence stop: 544.
 Location/Qualifiers

FEATURES
 source

1..573
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6559746"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC 126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AGCAGTGTATCAACGAGATGGCCATTACGCCGGG-3' and
 5'-ATTCAGAGCGGCGCGCGCATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC 127 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 573;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGCGCGCGGCAAGAG 60
 |||||
 Db 38 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGCGCGGCAAGAG 97
 |||||
 QY 61 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
 |||||
 Db 98 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGCCCTCTGGGCTGGGATATTGTGTTGAT 157
 |||||
 QY 121 AACTGTGCATCTGCGAGGAACACATATTGATCTTTGCATAGATGTCAAGCTTAACAG 180
 |||||
 Db 158 AACTGTGCATCTGCGAGGAACACATATTGATCTTTGCATAGATGTCAAGCTTAACAG 217
 |||||
 QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAACCATCTTTTAC 240
 |||||
 Db 218 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAACCATCTTTTAC 277
 |||||
 QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCATTGGACAACAGAG 300
 |||||
 Db 278 TTCACATGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCATTGGACAACAGAG 337
 |||||
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 |||||
 Db 338 TGGGAATTCAAAAGTATGGGCACTAG 364
 |||||

RESULT 34
 BP308845

LOCUS BP308845 591 bp mRNA linear EST 17-SEP-2004
 DEFINITION BP308845 Sugano cDNA library, brain Homo sapiens cDNA clone
 NRB06593, mRNA sequence.

ACCESSION BP308845
 VERSION BP308845.1 GI:52237818
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

REFERENCE 1 (bases 1 to 591)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

15342556
 Contact: Yutaka Suzuki

Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source

1..591
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NRB06593"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

ORIGIN

Query Match 100.0%; Score 327; DB 3; Length 591;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGCGCGGCAAGAG 60
 |||||
 Db 14 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGCGCGGCAAGAG 73
 |||||

QY 61 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
 |||||
 Db 74 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGCCCTCTGGGCTGGGATATTGTGTTGAT 133
 |||||

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QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 180
Db 134 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 193
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 194 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 253
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 300
Db 254 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 313
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 314 TGGGAATTCAAAAGTATGGGCACTAG 340

RESULT 35
BP3117451 583 bp mRNA linear EST 17-SEP-2004
LOCUS BP3117451 Sugano cDNA library, pericardium Homo sapiens cDNA clone
DEFINITION PCD03725, mRNA sequence.
ACCESSION BP3117451
VERSION BP3117451.1 GI:52246426
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Mizushima-Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD03725"
/tissue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN
Query Match 100.0%; Score 327; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 12 ATGGCGGCGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 71
QY 61 CGCTTTGAAGTGAAAGAGTGAATGCAATGAGTGTGGGCTGGGATATTTGGTTGAT 120
Db 72 CGCTTTGAAGTGAAAGAGTGAATGCAATGAGTGTGGGCTGGGATATTTGGTTGAT 131
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 180
Db 132 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 191
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 192 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 251
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 300

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Db 252 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 311
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 312 TGGGAATTCAAAAGTATGGGCACTAG 338

RESULT 36
BG705958 616 bp mRNA linear EST 07-MAY-2001
LOCUS BG705958 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792099 5',
DEFINITION mRNA sequence.
ACCESSION BG705958
VERSION BG705958.1 GI:13980825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 616)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10669 row: 1 column: 20
High quality sequence stop: 591.
Location/Qualifiers
1. 616
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792099"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 327; DB 2; Length 616;
Best Local Similarity 100.0%; Pred. No. 6.7e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGGCGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAAGAGTGAATGCAATGAGTGTGGGCTGGGATATTTGGTTGAT 120
Db 79 CGCTTTGAAGTGAAAGAGTGAATGCAATGAGTGTGGGCTGGGATATTTGGTTGAT 138
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 180
Db 139 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCTCAAGCTAACCG 198

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QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
 |||||
 Db 199 GCGTCCGCTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
 |||||
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCTCAATTCGACCAACAGAG 300
 |||||
 Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCTCAATTCGACCAACAGAG 318
 |||||
 QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
 |||||
 Db 319 TGGGAATTCCAAAGTATGGGCACTAG 345
 |||||

RESULT 37
 BG503311 NIH_MGC_61 736 bp mRNA linear EST 27-MAR-2001
 LOCUS 6025507221F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4658381 5',
 DEFINITION mRNA sequence.

ACCESSION BG503311
 VERSION BG503311.1 GI:13464828
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 736)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1452 row: i column: 06
 High quality sequence stop: 515.
 Location/Qualifiers

FEATURES

1..736
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4658381"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_61"
 /note="Torgan; testis; Vector: pDNR-LIB (Clontech); Site:1:
 SfII (ggcccttcggcc); Site:2: SfII (ggccattatggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGAGGCGGCACATG-dt(30)BN-3',
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 100.0%; Score 327; DB 2; Length 736;
 Best Local Similarity 100.0%; Pred. No. 6.7e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGGAGGATGGATGGATATCCCGAGCGGCACCAACAGCGGCGGGCAAGAG 60
 |||||
 Db 12 ATGGCGGAGGATGGATGGATATCCCGAGCGGCACCAACAGCGGCGGGCAAGAG 71
 |||||

QY 61 CGCTTTGAAGTGAAAAAGTCAGATGCACTAGCCCTCTCGGCTCGGATATTGTGTTGAT 120
 |||||
 Db 72 CGCTTTGAAGTGAAAAAGTCAGATGCACTAGCCCTCTCGGCTCGGATATTGTGTTGAT 131
 |||||
 QY 121 AACTGTGCCATCTCGCAGCAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 180
 |||||
 Db 132 AACTGTGCCATCTCGCAGCAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 191
 |||||
 QY 181 CGGTCCGCTACTTTCAGAAAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
 |||||
 Db 192 GGTTCGCTACTTTCAGAAAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 251
 |||||
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCTCAATTCGACCAACAGAG 300
 |||||
 Db 252 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGCTCAATTCGACCAACAGAG 311
 |||||
 QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
 |||||
 Db 312 TGGGAATTCCAAAGTATGGGCACTAG 338
 |||||

RESULT 38

BUS33420 801 bp mRNA linear EST 13-SEP-2002
 LOCUS AGENCOURT 10197966 NIH_MGC 126 Homo sapiens cDNA clone
 DEFINITION IMAGE:6559775 5', mRNA sequence.

ACCESSION BUS33420
 VERSION BUS33420.1 GI:22843861
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 801)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2731 row: i column: 23
 High quality sequence stop: 551.
 Location/Qualifiers

FEATURES

source

1..801
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6559775"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site:1: SfII (ggccattatggcc);
 Site:2: SfII (ggcccttcggcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGAGATGCGCATTCAGCGCGCG-3' and
 5'-ATTCTAGAGCCGAGGCGGCACATG-dt(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5-1
 kb size fraction (other fractions present in NIH_MGC 127
 and NIH_MGC 128). Library created in the laboratory of T.

Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN		Query Match	100.0%;	Score 327;	DB 5;	Length 801;
		Best Local Similarity	100.0%;	Pred. No. 6.8e-175;		
		Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCGGCACGGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGCGGCGCAAGAAG	60			
DB	44	ATGGCGGCACGGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGCGGCGCAAGAAG	103			
QY	61	CGCTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT	120			
DB	104	CGCTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT	163			
QY	121	AACGTGTGCCATCTGCAGGAACCAATATATGAAATCTTTGCATAGAAATGCTAAGCTTAACCAAG	180			
DB	164	AACGTGTGCCATCTGCAGGAACCAATATATGAAATCTTTGCATAGAAATGCTAAGCTTAACCAAG	223			
QY	181	CGCTCCGCTACTTTCAGAAAGATGTACTGTGCGCATGGGGAGTCTGTATACCATGCTTTTTCAC	240			
DB	224	CGCTCCGCTACTTTCAGAAAGATGTACTGTGCGCATGGGGAGTCTGTATACCATGCTTTTTCAC	283			
QY	241	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTTTGGACAAACAGAGAG	300			
DB	284	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTTTGGACAAACAGAGAG	343			
QY	301	TGGGAATTCCAAAAGTATGGGCACCTAG	327			
DB	344	TGGGAATTCCAAAAGTATGGGCACCTAG	370			

RESULT	39
BUS959349	
LOCUS	BUS959349 linear EST 21-OCT-2002
DEFINITION	845 bp mRNA Homo sapiens cDNA clone AGENCOURT 10623637 NIH MGC 127 Homo sapiens IMAGE:6737564 5'.. mrna sequence.

ACCESSION RU959349
 VERSION RU959349.1 GI:24188921
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 1 (bases 1 to 845)
 REFERENCE NTH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

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nttp://image.iimr.gov
Plate: LICM3067 row: m column: 19
High quality sequence stop: 424.
Location/Qualifiers
1..845
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6737564"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 127"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder

```

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACAGATGGCATTCAGCGGG-3' and 5'-ATTCTAGAGCGGAGCGGCCGATG-TT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC library."

ORIGIN		Query Match	100.0%; Score 327; DB 5; Length 845;
		Best Local Similarity 100.0%; Pred. No..6.e-175;	
	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGGCGCAGGATGGATGTGGATACCCGAGCGGCACCACAGCGCGCGGCAAGAAG	60
Db	22	ATGGCGCAGCATGGATGTGGATACCCGAGCGGCACCACAGCGCGCGGCAAGAAG	81
Qy	61	CGCTTTCAAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	120
Db	82	CGCTTTGAAGTAAAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	141
Qy	121	AACTGTGCCATCTCAGAGAACCAATTATGGATCTTTGCATAGATAATGTCAAGCTAACACAG	180
Db	142	AACTGTGCCATCTCAGAGAACCAATTATGGATCTTTGCATAGATAATGTCAAGCTAACACAG	201
Qy	181	GCGTTCGGCTACTTCAGAGAGAGTACTGTCCCATGGGGAGTCTGTAAACCATGCTTTTCAC	240
Db	202	GCGTTCGGCTACTTCAGAGAGTACTGTCCCATGGGGAGTCTGTAAACCATGCTTTTCAC	261
Qy	241	TTCCACTTGCATCTCTCGCTGGCTCAAAAACACGACAGGTGTGTCCAATTGGACAACAGAGAG	300
Db	262	TTCCACTTGCATCTCTCGCTGGCTCAAAAACACGACAGGTGTGTCCAATTGGACAACAGAGAG	321
Qy	301	TGGGAATTCCAAAAGTATGGGCACCTAG	327
Db	322	TGGGAATTCCAAAAGTATGGGCACCTAG	348

RESULT 40	886 bp	mRNA	linear	EST 21-MAR-2000
BG481544				
LOCUS	602528456P1	NIH_MGC_21	Homo sapiens	cDNA clone IMAGE:4652028 5',
DEFINITION	mRNA sequence.			
ACCESSION	BG481544			
VERSION	BG481544.1	GI:13413823		
KEYWORDS	EST.			
SOURCE	Homo sapiens	(human)		
ORGANISM	Homo sapiens			
REFERENCE	1. (bases 1 to 886)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI435 row: p column: 13 High quality sequence stop: 529.			

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FEATURES      Location/Qualifiers
  source      1..886
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4652028"
              /tissue_type="choriocarcinoma"
              /lab_host="NIH MGC 21"
              /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
              Site 2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Size-selected >500bp
              for average insert size 1.8kb. Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Query Match      100.0%; Score 327; DB 2; Length 886;
Best Local Similarity 100.0%; Pred. No. 6.8e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGTCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 60
Db 7 ATGGCGGCGAGTGGATGTCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 66
Qy 61 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 67 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 126
Qy 121 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCATAGAAATGTCAAGCTAACCA 180
Db 127 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCATAGAAATGTCAAGCTAACCA 186
Qy 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCC 240
Db 187 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCC 246
Qy 241 TTCCACTGTCATCTCTCGCTGCTCAAAACAGACAGGTGTGTCATTGGACAAACAGAG 300
Db 247 TTCCACTGTCATCTCTCGCTGCTCAAAACAGACAGGTGTGTCATTGGACAAACAGAG 306
Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGCACTAG 333
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RESULT 41

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BM459634
LOCUS      BM459634
DEFINITION AGENCOURT_6417786 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534260
5', mRNA sequence.
ACCESSION BM459634
VERSION    BM459634.1 GI:18508674
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 904)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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http://image.llnl.gov
Plate: LLM12220 row: h column: 05
High quality sequence stop: 684.

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FEATURES      Location/Qualifiers
  source      1..904
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5534260"
              /tissue_type="leiomyosarcoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_71"
              /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
              Average insert size 2.1 kb."
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ORIGIN

```

Query Match      100.0%; Score 327; DB 3; Length 904;
Best Local Similarity 100.0%; Pred. No. 6.8e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGTCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 60
Db 10 ATGGCGGCGAGTGGATGTCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 69
Qy 61 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 70 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 129
Qy 121 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCATAGAAATGTCAAGCTAACCA 180
Db 130 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGCATAGAAATGTCAAGCTAACCA 189
Qy 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCC 240
Db 190 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCC 249
Qy 241 TTCCACTGTCATCTCTCGCTGCTCAAAACAGACAGGTGTGTCATTGGACAAACAGAG 300
Db 250 TTCCACTGTCATCTCTCGCTGCTCAAAACAGACAGGTGTGTCATTGGACAAACAGAG 309
Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 310 TGGGAATTCCAAAGTATGGCACTAG 336
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RESULT 42

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BM459634
LOCUS      BM459634
DEFINITION AGENCOURT_7575192 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6049202
5', mRNA sequence.
ACCESSION BM459634
VERSION    BM459634.1 GI:20398138
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 945)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Plate: LLM13299 row: h column: 03

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 12:22:08 ; Search time 368.547 Seconds
(without alignments)
5913.368 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgagcgatggatgt.....tccaaagtatggcgactag 327

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 12

Total number of hits satisfying chosen parameters: 116703

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	327	3	AAA96882 Nucleotid
2	327	100.0	482	3	AAC03896 Human sec
3	327	100.0	506	12	ADQ87496 Human tum
4	327	100.0	506	12	ADQ87156 Human tum
5	327	100.0	506	13	ADQ84881 Human tum
6	327	100.0	508	3	AAA74978 Human encod
7	327	100.0	508	13	ACN40951 Tumour-as
8	325	99.4	476	9	ACH29979 Human tes
9	321	98.2	3726	13	ADS09913 Human tes
10	321	98.2	4543	11	ACN90161 Breast ca
11	320	97.9	503	12	ADQ92179 Human aut
12	308	94.2	4476	5	ABV25615 Human pro
13	296	90.5	311	14	ACL57420 Human col
14	296	90.5	3484	12	ADF42703 Human tes
15	296	90.5	3484	12	ADQ18564 Human sof
16	296	90.5	3484	13	ADQ80865 Human SPA
17	296	90.5	5111	10	ADB75558 Prostate
18	296	90.5	5371	12	ADQ23032 Human sof
19	267	81.7	5347	6	AAS94844 Human DNA

C	20	251	76.8	502	14	ADY78665
	21	249	76.1	3208	4	AAD12859
	22	209	63.9	509	5	AAS86845
	23	170	52.0	402	3	AAC06296
	24	170	52.0	439	9	ACH27559
	25	170	52.0	1482	3	AAC75216
	26	166	50.8	380	8	ABX39512
	27	149	45.6	666	5	AAS86844
	28	147	45.0	398	5	AAS86841
	29	131	40.1	358	5	AAS86842
	30	131	40.1	386	5	AAS86843
	31	99	30.3	416	5	AAS86840
	32	99	30.3	812	6	ABQ54871
	33	99	30.3	1478	12	ADJ72047
	34	90	27.5	346	4	AAL11142
	35	90	27.5	353	4	AAL18905
	36	89	27.5	415	11	ACN81343
	37	89	27.2	11301	4	AAK71591
	38	78	23.9	439	6	ABQ99527
	39	65	19.9	4099	5	AAS86847
	40	54	16.5	254	2	AAT26036
	41	50	15.3	504	3	AAA74980
	42	50	15.3	539	5	AAH97860
	43	50	15.3	557	5	AAH97861
	44	50	15.3	586	5	AAH97862
	45	40	12.2	416	4	AAI89292

ALIGNMENTS

RESULT 1

AAA96882

ID AAA96882 standard; DNA; 327 BP.

XX

AC AAA96882;

XX

DT 19-FEB-2001 (first entry)

XX

DE Nucleotide sequence of human ring finger protein ROC1.

XX

KW ROC1; ROC2; cullin; ring finger protein; APC1; APC complex; SCF pathway; cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation; tumour; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..327

FT /*tag= a

FT /product= "ROC1"

XX

PN WO200058472-A2.

XX

PD 05-OCT-2000.

XX

PF 31-MAR-2000; 2000WO-US008592.

XX

PR 31-MAR-1999; 99US-0127261P.

XX

PR 22-NOV-1999; 99US-0166927P.

XX

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Xiong Y, Ohta T;

XX

DR WPI; 2000-647235/62.

XX

DR P-PSDB; AAB19160.

XX

PT Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use.

XX

PS Claim 1; Fig 2A; 83pp; English.

XX The present sequence encodes a human ROC1 ring finger protein. The
CC specification also describes human ROC2. ROC1 and ROC2 are similar to
CC APC11, a subunit of the APC complex. The proteins stimulate cullin
CC dependent ubiquitin ligase activity. ROC1 functions in vivo as an
CC essential regulator of CDK inhibitor Sic1 degradation by the SCF
CC (undefined) pathway. ROC proteins are useful for screening bioactive
CC agents that interfere with the binding of ROC proteins with cullin
CC proteins. Pharmaceutical formulations comprising ROC proteins are useful
CC for diagnostic and therapeutic purposes, preferably for diagnosing and
CC treating tumours
XX
SQ Sequence 327 BP; 85 A; 75 C; 94 G; 73 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 3; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.6e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGCGGCAAG 60
DB 1 ATGGCGGCGAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGCGGCAAG 60
|||
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 120
DB 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 120
|||
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
DB 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
|||
QY 181 GCCTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 181 GCCTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
|||
QY 241 TTCACCTGCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAGAG 300
DB 241 TTCACCTGCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAGAG 300
|||
QY 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
DB 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
|||

RESULT 2
AAC03896
ID AAC03896 standard; cDNA; 482 BP.
XX AAC03896;
XX
XX
DT 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 3894.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EF1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX WPI; 2000-500381/45.
XX
XX P-PSDB; AAG03890.
XX

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 3894; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 482 BP; 116 A; 103 C; 121 G; 140 T; 0 U; 2 Other;

Query Match 100.0%; Score 327; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.6e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGCGGCAAG 60
DB 29 ATGGCGGCGAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGCGGCAAG 88
|||
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 120
DB 89 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 148
|||
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
DB 149 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 208
|||
QY 181 GCCTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 209 GCCTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 268
|||
QY 241 TTCACCTGCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAGAG 300
DB 269 TTCACCTGCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAGAG 328
|||
QY 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
DB 329 TGGGAATTCCTCAAAAGTATGGGCACCTAG 355
|||

RESULT 3
ADQ87496
ID ADQ87496 standard; cDNA; 506 BP.
XX ADQ87496;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
XX
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2004060270-A2.
XX
XX 22-JUL-2004.
XX
XX 15-OCT-2003; 2003WO-US029126.
XX

PR 18-OCT-2002; 2002US-0418988P.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 PI Wu TD, Zhou Y;
 XX
 XX WPI; 2004-534300/51.
 XX
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 XX
 PS Claim 1; SEQ ID NO 4374; 5504pp; English.
 XX
 CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide,
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a
 CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytostatic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.
 XX
 SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;
 Query Match 100.0%; Score 327; DB 12; Length 506;
 Best Local Similarity 100.0%; Pred. No. 2.6e-157;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCGGCGAGTGGATGTGGATATCCCGAGCGGACCAACAGCGCGGGGCAAGAAG 60
 Db 6 ATGGCGGCGAGTGGATGTGGATATCCCGAGCGGACCAACAGCGCGGGGCAAGAAG 65
 Qy 61 CGCTTTGAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 66 CGCTTTGAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
 Qy 121 AACTGTGCCATCTGCAGGACCAATATGATCTTTGCATAGATCTCAAGCTAACACAG 180
 Db 126 AACTGTGCCATCTGCAGGACCAATATGATCTTTGCATAGATCTCAAGCTAACACAG 185
 Qy 181 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGGAGTCTGTAACCATGCTTTTCAC 240

Db 186 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGGAGTCTGTAACCATGCTTTTCAC 245
 Qy 241 TTCACATGCGATCTCTCGCTGCTCAAAACACGACGAGTGTGTCATTGGGACAAACAGAGAG 300
 Db 246 TTCACATGCGATCTCTCGCTGCTCAAAACACGACGAGTGTGTCATTGGGACAAACAGAGAG 305
 Qy 301 TGGGAATTCCAAAGATATGGCACTAG 327
 Db 306 TGGGAATTCCAAAGATATGGCACTAG 332
 RESULT 4
 ID ADQ87156
 XX ADQ87156 standard; cDNA; 506 BP.
 AC ADQ87156;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
 XX
 KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 OS Homo sapiens.
 XX
 PN W02004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003WO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 XX Wu TD, Zhou Y;
 XX
 XX WPI; 2004-534300/51.
 XX
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 PS Claim 1; SEQ ID NO 4032; 5504pp; English.
 CC
 CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide,
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising

CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention

SQ Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.6e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 7 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 120
DB 67 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 126
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAATGTCAAGTCAACCAAG 180
DB 127 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAATGTCAAGTCAACCAAG 186
QY 181 GCGTCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCAATGCTTTTCAC 240
DB 187 GCGTCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCAATGCTTTTCAC 246
QY 241 TTCCACTGCAATCTCTCGCTGGCTCAAAACACAGCAGTGTGTCATTGGACACACAGAG 300
DB 247 TTCCACTGCAATCTCTCGCTGGCTCAAAACACAGCAGTGTGTCATTGGACACACAGAG 306
QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327
DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

RESULT 8
ACH29979

ID ACH29979 standard; cDNA; 476 BP.

AC ACH29979;

XX 13-OCT-2003 (first entry)

DT Human testis cDNA #365.

DE Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 17191; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX SQ Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

Query Match 99.4%; Score 325; DB 9; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.7e-156;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGGCGAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 62

DB 74 GGCGGCGAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 133

QY 63 CTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGTATAA 122

DB 134 CTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGTATAA 193

QY 123 CTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGTCAACAGGC 182

DB 194 CTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGTCAACAGGC 253

QY 183 GTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 242

DB 254 GTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 313

QY 243 CCACCTGCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACACAGAGATG 302

DB 314 CCACCTGCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACACAGAGATG 373

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

RESULT 9

ADS09913/C

ID ADS09913 standard; DNA; 3726 BP.

XX ADS09913;

XX 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 150.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

```
XX OS Homo sapiens.
XX PN WO2004080148-A2.
XX XX
XX PD 23-SEP-2004.
XX PF 30-SEP-2003; 2003WO-US030720.
XX PR 02-OCT-2002; 2002US-0416186P.
XX PA (NUVE-) NOVELO INC.
XX PI Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX DR MPI; 2004-668857/65.
XX DR P-PSDB; ADS10597.
XX XX
XX PT New polynucleotide, useful in preparing a composition for diagnosing or
XX PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX PT aplastic anemia or cancer for promoting wound healing.
XX PS Claim 1; SEQ ID NO 150; 718pp; English.
XX XX
XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic DNA of
XX CC the invention. The current sequence is not shown explicitly within the
XX CC specification but can be accessed from the WIPO web-site.
XX XX
XX SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
Query Match 98.2%; Score 321; DB 13; Length 3726;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
DB 492 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 433
QY 67 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATACTGT 126
DB 432 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATACTGT 373
QY 127 GCCATCTGCAGGAACCAACATTTATGGATCTTTGATAGAAATGCAAGCTAACCGGCTCC 186
DB 372 GCCATCTGCAGGAACCAACATTTATGGATCTTTGATAGAAATGCAAGCTAACCGGCTCC 313
QY 187 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 246
DB 312 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 253
QY 247 TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAA 306
DB 252 TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAA 193
QY 307 TTCCAAAGTATGGGCACTAG 327
DB 192 TTCCAAAGTATGGGCACTAG 172
RESULT 10
ACN90161/c
ID ACN90161 standard; DNA; 4543 BP.
XX AC
XX ACN90161;
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DT 02-DEC-2004 (first entry)
XX XX
XX DE Breast cancer related marker, seq id 11311.
XX XX
XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX XX
XX OS Homo sapiens.
XX PN US2003099974-A1.
XX PD 29-MAY-2003.
XX XX
XX PF 18-JUL-2002; 2002US-00198846.
XX PR 18-JUL-2001; 2001US-0306220P.
XX XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX XX
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX PI WPI; 2003-787014/74.
XX DR
XX XX
XX PT Novel isolated polypeptide associated with breast cancer, useful for
XX PT detecting presence of polypeptide in sample, as a marker for breast
XX PT cancer.
XX PS Disclosure; SEQ ID NO 11311; 36pp; English.
XX XX
XX CC The invention relates to an isolated polypeptide (I) associated with a
XX CC breast cancer which is encoded by a nucleic acid molecule comprising a
XX CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
XX CC the polypeptide of the invention. The activity of the polypeptide of the
XX CC invention may be described as cytostatic. The antibody is useful for
XX CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
XX CC invention are useful in the detection of breast tumours. (I) is useful as
XX CC a marker for breast cancer and in breast cancer therapy. Sequences given
XX CC in records ACN78851-ACN92934 represent nucleic acid markers associated
XX CC with breast cancer. Note: The sequence listing does not form part of the
XX CC specification but may be obtained in electronic format from the USPTO web
XX CC site at seqdata.uspto.gov/sequence.html?DocID=2003099974
XX XX
XX SQ Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
Query Match 98.2%; Score 321; DB 11; Length 4543;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
DB 1085 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 1026
QY 67 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATACTGT 126
DB 1025 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATACTGT 966
QY 127 GCCATCTGCAGGAACCAACATTTATGGATCTTTGATAGAAATGCAAGCTAACCGGCTCC 186
DB 965 GCCATCTGCAGGAACCAACATTTATGGATCTTTGATAGAAATGCAAGCTAACCGGCTCC 906
QY 187 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 246
DB 905 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 846
QY 247 TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAA 306
DB 845 TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGTGGGAA 786
QY 307 TTCCAAAGTATGGGCACTAG 327
DB 785 TTCCAAAGTATGGGCACTAG 765
RESULT 11
```

ADQ92179
ID ADQ92179 standard; DNA; 503 BP.
AC
XX
ADQ92179;
DT
XX 07-OCT-2004 (first entry)
DE Human autoantigen DNA fragment MPMGP800L05536.
XX
XX ds; autoantigen; antibody; hybridoma; biosensor chip;
KW extracorporeal differential diagnosis; autoimmune disease;
KW ribosomal protein; tubulin;
KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
KW affinity chromatography; electrophoresis; autoantibody apheresis;
KW RNA interference; RNAi.
XX
XX Homo sapiens.
OS
XX WO2004058972-A1.
PN
XX 15-JUL-2004.
PD
XX 23-DEC-2002; 2002WO-BP014731.
PF
XX 23-DEC-2002; 2002WO-BP014731.
PR
XX (THIE/) THIESEN H.
PA (LORE/) LORENZ P.
PA
XX Thiesen H, Lorenz P;
PI
XX WPI; 2004-543459/52.
DR
XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic
PT reagents and for treating autoimmune disease, also related expression
PT products and antibodies with similar uses.
PT
XX Claim 1; SEQ ID NO 160; 110pp; German.
PS
XX This invention describes novel human DNA autoantigens which are used to
CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;
CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express;
CC monoclonal Ab; biosensor chips having an addressable sequence pattern as
CC probes; medical or diagnostic instruments that include the biosensor; for
CC extracorporeal differential diagnosis of autoimmune diseases and
CC predileposition to them. The autoantigen polynucleotides encode ribosomal
CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl
CC transferases and proteins. The antibodies may be labelled conventionally
CC with radioisotopes, coloured or fluorescent groups, or a member of the
CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed
CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear
CC membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular
CC or basal membrane antigens; Golgi or cell nuclei, or associated with
CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope
CC mapping; in affinity chromatography or electrophoresis; for diagnosis,
CC prognosis, control of treatment or therapeutic response of autoimmune
CC diseases, particularly in vitro differential diagnosis of autoimmune
CC diseases; to produce biosensor chips or for autoantibody apheresis.
CC Autoantigen DNA can be used for therapeutic RNA interference against
CC autoantibodies. Biochips that carry the new materials are useful in
CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
XX autoantigens.
SQ Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;
Query Match 97.9%; Score 320; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1e-153;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGGGGCAAGCGCTTGG 67
DB 1 CAGCGATGGATGGGATACCCGAGCGGCACCAACAGCGCGGGGCAAGCGCTTGG 60

QY 68 AAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATGTGTTGATAACTGTG 127
DB 61 AAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATGTGTTGATAACTGTG 120
QY 128 CCATCTGCAGGAACCAACATTTATGGATCTTTGTCATAGAATGTCAAGCTAACACGCGTCCG 187
DB 121 CCATCTGCAGGAACCAACATTTATGGATCTTTGTCATAGAATGTCAAGCTAACACGCGTCCG 180
QY 188 CTACTTCAGAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
DB 181 CTACTTCAGAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 240
QY 248 GCATCTCTCGCTGGCTCAAAAACGACAGGTGTGTCCATTGGACAAACAGAGAGTGGGAAT 307
DB 241 GCATCTCTCGCTGGCTCAAAAACGACAGGTGTGTCCATTGGACAAACAGAGAGTGGGAAT 300
QY 308 TCCAAAAGTATGGGCACTAG 327
DB 301 TCCAAAAGTATGGGCACTAG 320
RESULT 12
ABV25615/c
ID ABV25615 standard; cDNA; 4476 BP.
XX
AC ABV25615;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25606.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5119-5120; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient

PR 04-JUN-2002; 2002US-0386107P.
PR 05-JUN-2002; 2002US-0386314P.
PR 05-JUN-2002; 2002US-0386326P.
PR 05-JUN-2002; 2002US-0386332P.
PR 05-JUN-2002; 2002US-0386481P.
PR 05-JUN-2002; 2002US-0386512P.
PR 05-JUN-2002; 2002US-0386513P.
PR 05-JUN-2002; 2002US-0386558P.
PR 05-JUN-2002; 2002US-0386600P.
PR 05-JUN-2002; 2002US-0386615P.
PR 05-JUN-2002; 2002US-0386615P.
PR 06-JUN-2002; 2002US-0386838P.
PR 06-JUN-2002; 2002US-0386861P.
PR 06-JUN-2002; 2002US-0386944P.
PR 06-JUN-2002; 2002US-0386955P.
PR 06-JUN-2002; 2002US-0387017P.
PR 06-JUN-2002; 2002US-0387026P.
PR 06-JUN-2002; 2002US-0387039P.
PR 20-JUN-2002; 2002US-0386865P.
XX
PA (META-) METABOLEX INC.
XX
XX Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;
XX
XX WPI; 2004-053469/05.
XX P-PSDB; ADF42704.
XX
PT Identifying an agent for treating diabetic or pre-diabetic individuals
PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,
PT and selecting an agent that modulates the expression or activity of the
PT polypeptide.
XX
XX Disclosure; SEQ ID NO 9; 209pp; English.
XX
XX The present invention describes a method for identifying an agent for
XX treating a diabetic or pre-diabetic individual. The method comprises
XX contacting an agent to a mixture comprising a polypeptide encoded by a
XX nucleic acid that hybridises under stringent conditions to a nucleic acid
XX encoding any of the 23 fully defined amino acid sequences given in the
XX specification, and selecting an agent that modulates the expression or
XX activity of the polypeptide. Also described: (1) a method of treating a
XX diabetic or pre-diabetic animal, comprising administering to the animal a
XX therapeutic amount of an agent identified by the method described above;
XX (2) a method of introducing an expression cassette into a cell,
XX comprising introducing into the cell an expression cassette comprising a
XX promoter operably linked to a polynucleotide encoding a polypeptide,
XX where the polynucleotide hybridises under stringent conditions to a
XX nucleic acid encoding the above amino acid sequences; and (3) a method of
XX diagnosing an individual who has Type 2 diabetes or is pre-diabetic,
XX comprising detecting in a sample from the individual the level of a
XX polypeptide or the level of the above-mentioned polynucleotide encoding
XX the polypeptide, where a modulated level of the polypeptide or
XX polynucleotide in the sample compared to a level of the polypeptide or
XX polynucleotide in either a lean individual or a previous sample from the
XX individual indicates that the individual is diabetic or pre-diabetic. The
XX method is useful in diagnosing and treating diabetes, insulin resistance
XX or related metabolic diseases in human subjects. The method may also be
XX used in identifying agents for treating diabetic or pre-diabetic
XX individuals. The present sequence is used in the exemplification of the
XX present invention.
XX
SQ Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;
Query Match 90.5%; Score 296; DB 12; Length 3484;
Best Local Similarity 100.0%; Pred. No. 2e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
Db 296 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 237
QY 67 GAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGT 126

Db 236 GAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGT 177
QY 127 GCATCTGCAGGAACCAACATTTATGATCTTTTCATAGAAATGTCAAGCTAACGAGCGTCC 186
Db 176 GCATCTGCAGGAACCAACATTTATGATCTTTTCATAGAAATGTCAAGCTAACGAGCGTCC 117
QY 187 GCTACTTCAAGAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCACTTCCAC 246
Db 116 GCTACTTCAAGAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCACTTCCAC 57
QY 247 TGCATCTCTCGTGGCTCAAAACACGACAGAGTGTGTCCATTGGACAACAGAGAGTG 302
Db 56 TGCATCTCTCGTGGCTCAAAACACGACAGAGTGTGTCCATTGGACAACAGAGAGTG 1
RESULT 15
ADQ18564/C
ID ADQ18564 standard; DNA; 3484 BP.
XX
XX AC ADQ18564;
XX
XX 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 1383.
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX
XX Example 2; SEQ ID NO 1383; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual,
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX DNA of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;
Query Match 90.5%; Score 296; DB 12; Length 3484;
Best Local Similarity 100.0%; Pred. No. 2e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66

Db 296 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGGCAAGAAGCGCTTT 237
Qy 67 GAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGATAAAGTGT 126
Db 236 GAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGATAAAGTGT 177
Qy 127 GCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAATGTCAAGCTAACCGGCGTCC 186
Db 176 GCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAATGTCAAGCTAACCGGCGTCC 117
Qy 187 GCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 246
Db 116 GCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 57
Qy 247 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAAACAGAGAGTG 302
Db 56 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAAACAGAGAGTG 1

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Job time : 372.547 secs

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GenCore version 5.1.7
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Word size : 12

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6: gb_pat.*
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8: gb_pr.*
9: gb_to.*
10: gb_sts.*
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13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	433	6 CQ698451	Sequence
3	327	100.0	453	6 CQ690099	Sequence
4	327	100.0	467	6 CQ695007	Sequence
5	327	100.0	471	6 CQ712328	Sequence
6	327	100.0	472	6 CQ711142	Sequence
7	327	100.0	482	6 BD027641	Sequence
8	327	100.0	482	6 AX888031	Sequence
9	327	100.0	507	6 CQ729899	Sequence
10	327	100.0	508	6 BD271520	VonHippel
11	327	100.0	508	6 AR640603	Sequence
12	327	100.0	508	6 AF140598	Homo sapi
13	327	100.0	523	6 CQ701366	Sequence
14	327	100.0	535	8 BC001466	Homo sapi
15	327	100.0	535	8 CR456560	Homo sapi
16	327	100.0	554	8 BC017370	Homo sapi
17	320	97.9	503	6 CQ832496	Sequence
18	308	94.2	497	8 HUMVQ60A05	Homo sapi

C	19	308	94.2	4476	6	CQ493737	Sequence
C	20	296	90.5	3484	8	HSTEST	X73608 H. sapiens m
	21	275	84.1	306	8	AY099360	Homo sapi
	22	270	82.6	468	6	CQ702730	Sequence
C	23	267	81.7	5347	6	AX281690	Sequence
	24	249	76.1	3208	6	AR277693	Sequence
	25	249	76.1	3208	6	AR542209	Sequence
	26	249	76.1	3208	6	AR651451	Sequence
	27	249	76.1	3208	6	AX212267	Sequence
	28	207	63.3	430	6	CQ709825	Sequence
	29	198	60.6	475	6	CQ705678	Sequence
	30	173	52.9	300	6	CQ703590	Sequence
	31	170	52.0	402	6	BD030041	Sequence
	32	170	52.0	402	6	AX894508	Sequence
	33	170	52.0	463	6	BD119236	EST and e
	34	170	52.0	463	6	AR423683	Sequence
	35	170	52.0	463	6	AX984377	Sequence
	36	163	49.8	370	6	CQ674921	Sequence
	37	157	48.0	318	6	CQ680807	Sequence
	38	148	45.3	486	6	CQ707821	Sequence
	39	141	43.1	450	6	CQ686479	Sequence
	40	132	40.4	135	6	CQ668705	Sequence
	41	124	37.9	325	6	CQ708874	Sequence
	42	99	30.3	363	6	CQ688757	Sequence
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	44	90	27.5	346	6	CQ418573	Sequence
	45	90	27.5	353	6	CQ426338	Sequence

ALIGNMENTS

RESULT 1	AF142059	Homo sapiens	327 bp	mrna	linear	PRI 14-JUL-1999
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DEFINITION	AF142059	Homo sapiens	327 bp	mrna	linear	PRI 14-JUL-1999
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VERSION	AF142059.1	GI:4809215				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
gene						
CDS						

Qy	1	ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGCGGCAAGAAG	60			
Db	17	ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGCGGCAAGAAG	76			
Qy	61	CGCTTTGAAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	120			
Db	77	CGCTTTGAAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	136			
Qy	121	AACGTGCGCCATCTGCAGGAAACCAATPATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG	180			
Db	137	AACGTGCGCCATCTGCAGGAAACCAATPATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG	196			
Qy	181	GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC	240			
Db	197	GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC	256			
Qy	241	TTCCACTGTCATCTCTCGCTGGCTCAAAAACAGCAGCAGGTGTGTCATTTGGACAACAGAGAG	300			
Db	257	TTCCACTGTCATCTCTCGCTGGCTCAAAAACAGCAGCAGGTGTGTCATTTGGACAACAGAGAG	316			
Qy	301	TGGGAATTCAAAAGTATGGGCACCTAG	327			
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LOCUS	CQ711142	472 bp	DNA			
DEFINITION	Sequence 56068 from Patent WO02070737.					
ACCESSION	CQ711142					
VERSION	CQ711142.1	GI:42271999				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Liew,C.C., Marshall,W.E. and Zhang,H.					
AUTHORS	Compositions and methods relating to osteoarthritis					
TITLE	Patent: WO 02070737-A 56068 12-SEP-2002;					
JOURNAL	Chondrogene Inc. (CA)					
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Qy	61	CGCTTTGAAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	120			
Db	80	CGCTTTGAAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	139			
Qy	121	AACGTGCGCCATCTGCAGGAAACCAATPATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG	180			
Db	140	AACGTGCGCCATCTGCAGGAAACCAATPATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG	199			
Qy	181	GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC	240			
Db	200	GCCTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC	259			
Qy	241	TTCCACTGTCATCTCTCGCTGGCTCAAAAACAGCAGCAGGTGTGTCATTTGGACAACAGAGAG	300			
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QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
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RESULT 7
BD027641
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/3887
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
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QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 120
Db 89 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 148

QY 121 AACTGTGCCATTCGAGGAACCAATATGGATCTTTGCGATGGGAGTCTGTAACCACTGTTTTCAC 180
Db 149 AACTGTGCCATTCGAGGAACCAATATGGATCTTTGCGATGGGAGTCTGTAACCACTGTTTTCAC 208

QY 181 GCGTCCGCTACTTCAGAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 240
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QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACAACAGAG 300
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QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
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RESULT 8
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/3887
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
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QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
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QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 120
Db 89 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 148

QY 121 AACTGTGCCATTCGAGGAACCAATATGGATCTTTGCGATGGGAGTCTGTAACCACTGTTTTCAC 180
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QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
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Best Local Similarity 100.0%; Pred. No. 3.6e-184;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
Db 29 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 88

QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 120
Db 89 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 148

QY 121 AACTGTGCCATTCGAGGAACCAATATGGATCTTTGCGATGGGAGTCTGTAACCACTGTTTTCAC 180
Db 149 AACTGTGCCATTCGAGGAACCAATATGGATCTTTGCGATGGGAGTCTGTAACCACTGTTTTCAC 208

QY 181 GCGTCCGCTACTTCAGAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 240
Db 209 GCGTCCGCTACTTCAGAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 268

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACAACAGAG 300
Db 269 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACAACAGAG 328

QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 329 TGGGAATTCCAAAGTATGGGCACTAG 355

RESULT 9
CQ729899
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
CQ729899
Sequence 15833 from Patent WO02068579.
CQ729899
CQ729899.1 GI:42302243
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
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Db      67  CGCTTTGAAGTGAAGAATGCAATAGCAGTAGCCCTCTGGGCCCTGGGATATTGTTGGTTGAT 126
QY      121  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 180
Db      127  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 186
QY      181  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db      187  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 246
QY      241  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 300
Db      247  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 306
QY      301  TGGGAATTCCAAAGTATGGGCACTAG 327
Db      307  TGGGAATTCCAAAGTATGGGCACTAG 333

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RESULT 12
AF140598
LOCUS      Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
DEFINITION
ACCESSION AF140598
VERSION    AF140598.1 GI:4769003
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE 1 (bases 1 to 508)
AUTHORS   Kamura,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J.,
            Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
            Conaway,R.C., Harper,J.W., and Conaway,J.W.
            RBX1, a component of the VHL tumor suppressor complex and SCF
            ubiquitin ligase
            Science 284 (5414), 657-661 (1999)
PUBMED    10213691
REFERENCE 2 (bases 1 to 508)
AUTHORS   Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
            Direct Submission
            Submitted (05-APR-1999) Prog. Molec. Cell Biol., HMI, Oklahoma
            Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
            Location/Qualifiers
            1..508
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            1..508
            /gene="RBX1"
            7..333
            /gene="RBX1"
            /note="ring finger-like protein; component of VHL tumor
            suppressor complex and SCF ubiquitin ligase"
            /codon_start=1
            /product="ring-box protein 1"
            /protein_id="AAD29715.1"
            /db_xref="GI:4769004"
            /translation="MAAAMDVTPSGTNSGAGKKRFEVKKNVAVALWAMDIVVDNCAI
            CRNHMDLICQANQASATSEECTVAVGNCNHFPHFICISRLKTRQVCPLDNREME
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ORIGIN
Query Match      100.0%; Score 327; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 3.6e-184;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGCGGACGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGGCAAGAAG 60
Db      7  ATGGCGGACGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGGCAAGAAG 66

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QY      61  CGCTTTGAAGTGAAGAATGCAATAGCAGTAGCCCTCTGGGCCCTGGGATATTGTTGGTTGAT 120
Db      67  CGCTTTGAAGTGAAGAATGCAATAGCAGTAGCCCTCTGGGCCCTGGGATATTGTTGGTTGAT 126
QY      121  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 180
Db      127  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 186
QY      181  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db      187  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 246
QY      241  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 300
Db      247  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 306
QY      301  TGGGAATTCCAAAGTATGGGCACTAG 327
Db      307  TGGGAATTCCAAAGTATGGGCACTAG 333

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RESULT 13
CQ701366
LOCUS      Homo sapiens
DEFINITION Sequence 46292 from Patent WO02070737.
ACCESSION CQ701366
VERSION    CQ701366.1 GI:42262133
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE 1
AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE      Compositions and methods relating to osteoarthritis
JOURNAL    Patent: WO 02070737-A 46292 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
            source
            1..523
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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ORIGIN
Query Match      100.0%; Score 327; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 3.6e-184;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGCGGACGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGGCAAGAAG 60
Db      19  ATGGCGGACGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGGCAAGAAG 78
QY      61  CGCTTTGAAGTGAAGAATGCAATAGCAGTAGCCCTCTGGGCCCTGGGATATTGTTGGTTGAT 120
Db      79  CGCTTTGAAGTGAAGAATGCAATAGCAGTAGCCCTCTGGGCCCTGGGATATTGTTGGTTGAT 138
QY      121  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 180
Db      139  AACTGTGCCATCTGCAGGAACCAACATTATGGATCTTTTGCATAGAATGTCAAGCTAACCCAG 198
QY      181  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db      199  GCGTCGCTACTTTCAGAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC 258
QY      241  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 300
Db      259  TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACACACAGAG 318
QY      301  TGGGAATTCCAAAGTATGGGCACTAG 327
Db      319  TGGGAATTCCAAAGTATGGGCACTAG 345

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ZK287.5

The location of this clone is unknown.

FEATURES
source

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="IMAGES:200144"

/db_xref="taxon:9606"

/clone_lib="Soares_fetal_liver_spleen_INFLS"

3. .305

/notes="similar to Caenorhabditis elegans protein Z70757"

(PID:g1262999)"

18. .284

/notes="similar to Caenorhabditis elegans protein U80449"

(PID:g1707068)"

36. .302

/notes="similar to Saccharomyces cerevisiae protein S66830"

(PID:g2132017)"

42. .302

/notes="similar to Schizosaccharomyces pombe protein Z98977"

(PID:g2388937)"

51. .284

/notes="similar to Caenorhabditis elegans protein Z46242"

(PID:g559430)"

ORIGIN

Query Match 94.2%; Score 308; DB 8; Length 497;

Best Local Similarity 100.0%; Pred. No. 9.1e-173;

Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20

TTGATATCCCGAGCGGACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGAAGT 79

DB 1

TTGATATCCCGAGCGGACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGAAGT 60

QY 80

GGATGAGTATGATGCTTGGGCTGGGATATTTGGTTGATTAATGTCATCTGCAGGA 139

DB 61

GGATGAGTATGATGCTTGGGCTGGGATATTTGGTTGATTAATGTCATCTGCAGGA 120

QY 140

ACCACATATGATGATCTTTGCATAGATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 199

DB 121

ACCACATATGATGATCTTTGCATAGATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 180

QY 200

AGTGTACTGTGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 259

DB 181

AGTGTACTGTGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 240

QY 260

GGCTCAAAACACGACAGTGTGTCATTGGACACAGAGATGGGAATTCAAAAGTATG 319

DB 241

GGCTCAAAACACGACAGTGTGTCATTGGACACAGAGATGGGAATTCAAAAGTATG 300

QY 320

GGCACTAG 327

DB 301

GGCACTAG 308

RESULT 19

CQ493737/c

LOCUS

Sequence 25604 from Patent WO0160860.

ACCESSION

CQ493737

VERSION

CQ493737.1 GI:41459356

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

Schlegel R., Endege W.O. and Monahan J.E.

Genes differentially expressed in human prostate cancer and their

use

JOURNAL

Patent: WO 0160860-A 25604 23-AUG-2001;

Millennium Predictive Medicine, Inc. (US)

FEATURES
source

Location/Qualifiers

1. .4476

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 94.2%; Score 308; DB 6; Length 4476;

Best Local Similarity 100.0%; Pred. No. 9.9e-173;

Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7

GCAGCGATGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGTTT 66

DB 1014

GCAGCGATGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGTTT 955

QY 67

GAAGTCAAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATAACTGT 126

DB 954

GAAGTCAAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATAACTGT 895

QY 127

GCATCTGCAGGACACACATTTGATCTTTGATAGATTCGAAGTACCAAGTACCAAGCGTCC 186

DB 894

GCATCTGCAGGACACACATTTGATCTTTGATAGATTCGAAGTACCAAGTACCAAGCGTCC 835

QY 187

GCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCAC 246

DB 834

GCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCAC 775

QY 247

TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAA 306

DB 774

TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAA 715

QY 307

TTCCAAAA 314

DB 714

TTCCAAAA 707

RESULT 20

HSTEST/c

LOCUS

H. sapiens mRNA for testican.

DEFINITION

X73608

ACCESSION

X73608.1 GI:793844

VERSION

testican.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 3484)

Allioli, P.M., Perin, J.P., Jolles, P. and Bonnet, F.J.

Testican, a multidomain testicular proteoglycan resembling

modulators of cell social behaviour

JOURNAL

Eur. J. Biochem. 214 (1), 347-350 (1993)

PUBMED

8389704

FEATURES

source

Location/Qualifiers

1. .3484

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone_lib="lambda gt11"

435. .1754

/codon_start=1

/product="testican"

/protein_id="CAA51999.1"

/db_xref="GI:793845"

/db_xref="GOA:Q08629"

/db_xref="InterPro:IPR000716"

/db_xref="UniProt/Swiss-Prot:Q08629"

/translation="MPAIVLAAAAAAMCFDQVSHRLDALAGAGNHNFLNDQW

LSTVSYDRDDKYNNRFRDDYDFRNWPNKPFQDALDPSKDPCLKVKCSHPKVCVTQDY

QTALCVSRKHLIPROKKGNVAQKHVGPNSLVKCPKCPVAQSAVCSGSDGHSYTSCKK

LEFHACSTGKSLATLDCGPCPLPEPPPKHAERSACTDKELRNLASRLKDWFGALH

RESULT 26
AR651451
LOCUS AR651451 3208 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 27 from patent US 6881563.
ACCESSION AR651451
VERSION AR651451.1 GI:62795924
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3208)
AUTHORS Donoho,G., Scoville,J., Turner,C.A. Jr., Friedrich,G., Abuin,A.,
Zambrowicz,B. and Sands,A.T.
TITLE Human proteases and polynucleotides encoding the same
JOURNAL Patent: US 6881563-A 27 19-APR-2005;
Lexicon Genetics Incorporated; The Woodlands, TX
FEATURES
source
1..3208
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 76.1%; Score 249; DB 6; Length 3208;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 TGGNATGCAGTACCCCTCTGGGCTGGGATATTGTTGATTAACCTGTCATCTGCAGG 138
DB 2776 TGGNATGCAGTACCCCTCTGGGCTGGGATATTGTTGATTAACCTGTCATCTGCAGG 2835
QY 139 AACACATTATGGATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 198
DB 2836 AACACATTATGGATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 2895
QY 199 GAGTGTACTTGCATCGGAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTTGCATCGGAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGC 2955
QY 259 TGGCTCAAAACACGACAGGTGTGCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACGACAGGTGTGCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 3015
QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

RESULT 27
AX212267
LOCUS AX212267 3208 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 27 from Patent W00159134.
ACCESSION AX212267
VERSION AX212267.1 GI:15524031
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Donoho,G., Scoville,J., Turner,C.A., Friedrich,G.B., Abuin,A.,
Zambrowicz,B. and Sands,A.T.
TITLE Human proteases and polynucleotides encoding the same
JOURNAL Patent: W0 0159134-A 27 16-AUG-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source
1..3208
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.1%; Score 249; DB 6; Length 3208;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 TGGNATGCAGTACCCCTCTGGGCTGGGATATTGTTGATTAACCTGTCATCTGCAGG 138
DB 2776 TGGNATGCAGTACCCCTCTGGGCTGGGATATTGTTGATTAACCTGTCATCTGCAGG 2835
QY 139 AACACATTATGGATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 198
DB 2836 AACACATTATGGATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 2895
QY 199 GAGTGTACTTGCATCGGAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTTGCATCGGAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGC 2955
QY 259 TGGCTCAAAACACGACAGGTGTGCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACGACAGGTGTGCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 3015
QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024
RESULT 28
CQ709825
LOCUS CQ709825 430 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 54751 from Patent W002070737.
ACCESSION CQ709825
VERSION CQ709825.1 GI:42270679
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.B. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: W0 02070737-A 54751 12-SEP-2002;
ChondroGene Inc. (CA)
FEATURES
source
1..430
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 63.3%; Score 207; DB 6; Length 430;
Best Local Similarity 99.7%; Pred. No. 3.8e-112;
Matches 327; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 21 ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 80
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 81 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 140
QY 121 AACTGTGCCATCTGCAGGAACCACTTATGGATCTTTGATAGATCTCAAGCTAA-CCA 179
DB 141 AACTGTGCCATCTGCAGGAACCACTTATGGATCTTTGATAGATCTCAAGCTAA-CCA 200
QY 180 GGCCTCCGCTACTTTCAGAGAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTTCA 239
DB 201 GGCCTCCGCTACTTTCAGAGAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTTCA 260
QY 240 CTTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGA 299
DB 261 CTTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGA 320


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Db 226 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 275
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RESULT 32
AX894508
LOCUS AX894508 402 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10371 from Patent EP1033401.
ACCESSION AX894508
VERSION AX894508.1 GI:40049392
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 10371 06-SEP-2000;
Genset (FR)
FEATURES
source Location/Qualifiers
1..402
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 52.0%; Score 170; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.2e-90;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 217
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Db 106 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 165
|||||

Qy 218 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 277
|||||
Db 166 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 225
|||||

Qy 278 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 327
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Db 226 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 275
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RESULT 33
BD119236
LOCUS BD119236 463 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD119236
VERSION BD119236.1 GI:23214146
KEYWORDS JP 2002010789-A/11313.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 463)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
EST and encoded human protein
Patent: JP 2002010789-A 11313 15-JAN-2002;
GENSET CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/11313
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00

|||||
CC n=a, g, c or t Location/Qualifiers
FH Key 74.
FT misc Location/Qualifiers
1..463
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/db_xref="taxon:9606"

FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match 52.0%; Score 170; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.3e-90;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 217
|||||
Db 101 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 160
|||||

Qy 218 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 277
|||||
Db 161 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 220
|||||

Qy 278 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 327
|||||
Db 221 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 270
|||||

RESULT 34
AR423683
LOCUS AR423683 463 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15180 from patent US 6639063.
ACCESSION AR423683
VERSION AR423683.1 GI:40178793
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 463)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 15180 28-OCT-2003;
Genset S.A.;;
WOX;
FEATURES
source Location/Qualifiers
1..463
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 52.0%; Score 170; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.3e-90;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 217
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Db 101 GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG 160
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Qy 218 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 277
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Db 161 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG 220
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Qy 278 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 327
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Db 221 TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG 270
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RESULT 35
AX984377
LOCUS AX984377 463 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 15180 from Patent EP1104808.
ACCESSION AX984377
VERSION AX984377.1 GI:40990517
KEYWORDS
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Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 96 CTGGSCCTGGGATATTGGTTGATTAAGTCCATCTGCAGGACACACATTATGGATCT 155
Db 91 CTGGSCCTGGGATATTGGTTGATTAAGTCCATCTGCAGGACACACATTATGGATCT 150
Qy 156 TTGCATAGAATGTCAAGCTAACCAAGCGGTCCGCTACTTTCAGAAGAGTGTACTGTCGCATG 215
Db 151 TTGCATAGAATGTCAAGCTAACCAAGCGGTCCGCTACTTTCAGAAGAGTGTACTGTCGCATG 210
Qy 216 GGGAGTCTGTAAACCATGCTTTTCACTTC 243
Db 211 GGGAGTCTGTAAACCATGCTTTTCACTTC 238

RESULT 39
LOCUS CQ686479 450 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 31405 from Patent WO02070737.
ACCESSION CQ686479
VERSION CQ686479.1 GI:42215585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 31405 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.6e-72;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 158 GCATAGAATGTCAAGCTAACCAAGCGGTCCGCTACTTTCAGAAGAGTGTACTGTCGCATGGG 217
Db 109 GCATAGAATGTCAAGCTAACCAAGCGGTCCGCTACTTTCAGAAGAGTGTACTGTCGCATGGG 168
Qy 218 GAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACGACAGG 277
Db 169 GAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACGACAGG 228
Qy 278 TGTGTCCATTGGACAACAGAG 298
Db 229 TGTGTCCATTGGACAACAGAG 249

RESULT 40
LOCUS CQ688705 135 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 13631 from Patent WO02070737.
ACCESSION CQ688705
VERSION CQ688705.1 GI:42157083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 13631 12-SEP-2002;
Chondrogene Inc. (CA)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGCAGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGCAAGAAG 60
Db 4 ATGGCGGCAGCGATGGATGGATACCCCGAGCGGCACCAACACGCGCGGCAAGAAG 63
Qy 61 CGCTTTGAAGTGAAGATGGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 120
Db 64 CGCTTTGAAGTGAAGATGGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 123
Qy 121 AACTGTGCCATC 132
Db 124 AACTGTGCCATC 135

RESULT 41
LOCUS CQ708874 325 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 53800 from Patent WO02070737.
ACCESSION CQ708874
VERSION CQ708874.1 GI:42269668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 53800 12-SEP-2002;
Chondrogene Inc. (CA)
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Db 82 GCATAGAATGTCAAGCTAACCAAGCGGTCCGCTACTTTCAGAAGAGTGTACTGTCGCATGGG 141
Qy 218 GAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACGACAGG 277
Db 142 GAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACGACAGG 201
Qy 278 TGTG 281
Db 202 TGTG 205

RESULT 42
LOCUS CQ688757 363 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 33683 from Patent WO02070737.
ACCESSION CQ688757
VERSION CQ688757.1 GI:42221728
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Liew C.C., Marshall, W.E. and Zhang, H.
AUTHORS Compositions and methods relating to osteoarthritis
TITLE Patent: WO 02070737-A 33683 12-SEP-2002;
JOURNAL Chondrogene Inc. (CA)
FEATURES Location/Qualifiers
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 93 CATGCTTTTCACCTCCACTGCATCTCTCGCTGCTCAAAACACGACGAGGTGTGCCATTG 152
QY 289 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 327
Db 153 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 191
RESULT 43
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LOCUS AK090764 1871 bp mRNA linear PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ33445 fis, clone BRALZ2000263.
ACCESSION AK090764
VERSION AK090764.1 GI:21748986
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
AUTHORS Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, S., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Teraehima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
Neguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isoqai, T. and Sugano, S.
TITLE Complete sequencing and characterization of 21,243 full-length
human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isoqai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1871)
Isoqai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isoqai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES Location/Qualifiers
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/clone_lib="BRALZ2"
/note="cloning vector: pME18SFL3"
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Query Match 30.3%; Score 99; DB 8; Length 1871;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 CATGCTTTTCACCTCCACTGCATCTCTCGCTGCTCAAAACACGACGAGGTGTGCCATTG 288
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QY 289 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 327
Db 1659 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 1697
Search completed: March 15, 2006, 18:00:43
Job time : 2416 secs

Result No.	Score	Query		DB	ID	Description	
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1	327	100.0	433	7	US-10-242-535A-43377	Sequence 43377, A	
2	327	100.0	433	7	US-10-085-783A-43377	Sequence 43377, A	
3	327	100.0	453	7	US-10-242-535A-35025	Sequence 35025, A	
4	327	100.0	453	7	US-10-085-783A-35025	Sequence 35025, A	
5	327	100.0	467	7	US-10-242-535A-39933	Sequence 39933, A	
6	327	100.0	467	7	US-10-085-783A-39933	Sequence 39933, A	
7	327	100.0	471	7	US-10-242-535A-57254	Sequence 57254, A	
8	327	100.0	471	7	US-10-085-783A-57254	Sequence 57254, A	
9	327	100.0	472	7	US-10-242-535A-56068	Sequence 56068, A	
10	327	100.0	472	7	US-10-085-783A-56068	Sequence 56068, A	
11	327	100.0	508	8	US-10-913-937-3	Sequence 3, Appl	
12	327	100.0	523	7	US-10-242-535A-46292	Sequence 46292, A	
13	327	100.0	523	7	US-10-085-783A-46292	Sequence 46292, A	
14	325	99.4	476	3	US-09-918-995-17191	Sequence 17191, A	
c	15	321.8	98.4	4543	5	US-10-198-846-11311	Sequence 11311, A
	16	316	96.6	430	7	US-10-242-535A-54751	Sequence 54751, A
c	17	316	96.6	4470	8	US-10-085-783A-54751	Sequence 54751, A
	18	308.8	94.4	4476	8	US-10-357-930-25604	Sequence 25604, A
19	302.4	92.5	380	3	US-09-960-352-4677	Sequence 4677, Ap	
c	20	301.2	92.1	5347	6	US-10-240-955-99	Sequence 99, Appl
c	21	296.8	90.8	3484	8	US-10-723-860-1383	Sequence 1383, Ap
c	22	296.8	90.8	3484	9	US-10-756-149-1357	Sequence 1357, Ap
c	23	296.8	90.8	5111	5	US-10-205-823-382	Sequence 382, App

241 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACACAGAG 300
Db 260 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACACAGAG 319
Qy 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 2
US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-43377

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Best Local Similarity 100.0%; Pred. No. 5.4e-104;
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Db 324 TGGGAATTCAAAAGTATGGGCACTAG 350

RESULT 4
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; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
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; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

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Qy 241 TTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACACAGAG 300
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Qy 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 3
US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
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US-10-085-783A-43377

Query Match 100.0%; Score 327; DB 7; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.4e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 20 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
Qy 121 AACTGTGCCATCTCGAGAACCAATATGATGATCTTTGATAGATCTCAAGCTAACCCAG 180
Db 140 AACTGTGCCATCTCGAGAACCAATATGATGATCTTTGATAGATCTCAAGCTAACCCAG 199
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RESULT 3
US-10-085-783A-35025
; Sequence 35025, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005

Best Local Similarity 100.0%; Pred. No. 5.5e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
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; Sequence 39933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 20 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 121 AACTGTGCGCATCTGCAGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCG 180
DB 140 AACTGTGCGCATCTGCAGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCG 199
QY 181 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 204 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 259
QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 300
DB 264 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 323
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
DB 324 TGGGAATTCAAAAGTATGGGCACTAG 350

Db 200 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCAC 259
QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 300
DB 260 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 319
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
DB 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 6
US-10-085-783A-39933
; Sequence 39933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 20 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 121 AACTGTGCGCATCTGCAGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCG 180
DB 140 AACTGTGCGCATCTGCAGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCG 199
QY 181 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 200 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 259
QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 300
DB 260 TTCACATGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 319
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
DB 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 7
US-10-242-535A-57254
; Sequence 57254, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

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; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-57254

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Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
   |||||||
Db 17 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
   |||||||
QY 61 CGCTTTGAAGTGAAGAGTGAATGCAATGATGAGTCTGGGCTGGGATATTTGGTTGAT 120
   |||||||
Db 77 CGCTTTGAAGTGAAGAGTGAATGCAATGATGAGTCTGGGCTGGGATATTTGGTTGAT 136
   |||||||
QY 121 AACTGTGCCATCTGCAGGAACCAATATGATGATCTTTGATAGATGTCAGCTAACCCAG 180
   |||||||
Db 137 AACTGTGCCATCTGCAGGAACCAATATGATGATCTTTGATAGATGTCAGCTAACCCAG 196
   |||||||
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
   |||||||
Db 197 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 256
   |||||||
QY 241 TTCCACTGCACTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACACAGAGAG 300
   |||||||
Db 257 TTCCACTGCACTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACACAGAGAG 316
   |||||||
QY 301 TGGGAATTCAGAAAGTATGGGCACTAG 327
   |||||||
Db 317 TGGGAATTCAGAAAGTATGGGCACTAG 343
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RESULT 8
US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-57254

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Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
   |||||||
Db 17 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
   |||||||
QY 61 CGCTTTGAAGTGAAGAGTGAATGCAATGATGAGTCTGGGCTGGGATATTTGGTTGAT 120
   |||||||
Db 77 CGCTTTGAAGTGAAGAGTGAATGCAATGATGAGTCTGGGCTGGGATATTTGGTTGAT 136
   |||||||
QY 121 AACTGTGCCATCTGCAGGAACCAATATGATGATCTTTGATAGATGTCAGCTAACCCAG 180
   |||||||
Db 137 AACTGTGCCATCTGCAGGAACCAATATGATGATCTTTGATAGATGTCAGCTAACCCAG 196
   |||||||
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
   |||||||
Db 197 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 256
   |||||||
QY 241 TTCCACTGCACTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACACAGAGAG 300
   |||||||
Db 257 TTCCACTGCACTCTCGCTGGCTCAAAACACGACGAGTGTGTCATTGGACACAGAGAG 316
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QY 301 TGGGAATTCAGAAAGTATGGGCACTAG 327
   |||||||
Db 317 TGGGAATTCAGAAAGTATGGGCACTAG 343
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RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-56068

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Query Match      100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
   |||||||
Db 20 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
   |||||||
QY 61 CGCTTTGAAGTGAAGAGTGAATGCAATGATGAGTCTGGGCTGGGATATTTGGTTGAT 120
   |||||||

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Db 80 CGCTTTGAAGTCAAAAAGTGAATGAGTACCTCTGGGCTGGGATATTGTGGTTGAT 139
Qy 121 AACTGTGCACTCTGAGGAACACACATTATGATCTTTTCATAGATATGCTCAAGCTAACCAAG 180
Db 140 AACTGTGCACTCTGAGGAACACACATTATGATCTTTTCATAGATATGCTCAAGCTAACCAAG 199
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTCTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAGAGTGTACTCTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 259
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 319
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGGCACTAG 346

RESULT 10

US-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGGGCGGGCAAGAG 60
Db 20 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGGGCGGGCAAGAG 79
Qy 61 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGAT 120
Db 80 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGAT 139
Qy 121 AACTGTGCCATCTCAGGAACCAACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG 180
Db 140 AACTGTGCCATCTCAGGAACCAACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG 199
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 259

Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 319
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGGCACTAG 346

RESULT 11

US-10-913-937-3
; Sequence 3, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGGGCGGGCAAGAG 60
Db 7 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGGGCGGGCAAGAG 66
Qy 61 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGAT 120
Db 67 CGCTTTGAAGTGAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGAT 126
Qy 121 AACTGTGCCATCTCAGGAACCAACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG 180
Db 127 AACTGTGCCATCTCAGGAACCAACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCAAG 186
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCAATGGGAGTCTGTAAACCATGCTTTTTCAC 246
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGACAGGTGTGTCCATTGGACAAACAGAGAG 306
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGGCACTAG 333

RESULT 12

US-10-242-535A-46292
; Sequence 46292, Application US/10242535A

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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.9e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 198
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAG 318
QY 301 TGGGAATTCGAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCGAAAGTATGGGCACTAG 345

RESULT 14
US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-17191

Query Match      99.4%; Score 325; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.9e-103;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 62
Db 74 GCGCGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 133
QY 63 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 122
Db 134 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 193
QY 123 CTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGGC 182
Db 123 CTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGGC 182
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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.9e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGGCAGCGATGGATGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 198
QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAG 318
QY 301 TGGGAATTCGAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCGAAAGTATGGGCACTAG 345

RESULT 13
US-10-085-783A-46292
; Sequence 46292, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
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Search completed: March 8, 2006, 17:28:04
Job time : 661.377 secs

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Result No.	Score	Query			DB ID	Description
		Match	Length			
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2	177.2	54.2	693	9	US-11-096-568A-26820	Sequence 26820, A
3	172.4	52.7	348	9	US-11-096-568A-28569	Sequence 28569, A
4	169.8	51.9	432	9	US-11-096-568A-14405	Sequence 14405, A
5	130	39.8	366	7	US-10-932-182A-2279	Sequence 2279, Ap
6	130	39.8	366	7	US-10-932-182A-2279	Sequence 2279, Ap
7	123.6	37.8	366	7	US-10-932-182A-78459	Sequence 78459, A
8	123.6	37.8	366	7	US-10-932-182A-78459	Sequence 78459, A
9	76	23.2	342	8	US-10-821-234-554	Sequence 554, App
c 10	74	22.6	153	7	US-10-932-182A-81177	Sequence 81177, A
c 11	74	22.6	153	7	US-10-932-182A-81177	Sequence 81177, A
c 12	68.2	20.9	546	12	US-11-128-061-5740	Sequence 5740, Ap
c 13	68.2	20.9	546	12	US-11-128-049-5740	Sequence 5740, Ap
c 14	68.2	20.9	579	12	US-11-128-061-2098	Sequence 2098, Ap
c 15	68.2	20.9	579	12	US-11-128-049-2098	Sequence 2098, Ap
c 16	65.4	20.0	207	7	US-10-932-182A-6146	Sequence 6146, Ap
c 17	65.4	20.0	207	7	US-10-932-182A-6146	Sequence 6146, Ap
c 18	42.8	13.1	450	9	US-11-057-484A-14	Sequence 14, Appl
c 19	39.6	12.1	3404	12	US-11-045-468A-18	Sequence 18, Appl
c 20	34.2	10.5	201	8	US-10-995-561-20992	Sequence 20992, A


```

US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

Query Match          39.8%; Score 130; DB 7; Length 366;
Best Local Similarity 68.0%; Pred. No. 2.6e-31;
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0

QY      55 AAGAAGCGCTTTGAAGTGA AAAAGTGGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTG 114
DB      94 AAAAAAAGATTTCGAGATTAAATAATGGACGGTGGCGTTCTGCTGCTGGGATATAGCC 153

QY      115 GTTGATAACTGTGCCATCTGCAGNACCACATATTGGAATCTTTGGCATAGAAATGTCAGACT 174
DB      154 GTTGACAACATGTGCCATTTCGAGAAACCACATATTGGAACCAATGCATCGAATGCCAGCGC 213

QY      175 AACCAGGCGTCGCTACTTTCAGAGAGTGTA CTGTCGATCGGGAGTCTGTAAACCATGCT 234
DB      214 AAGCTATGACCGACACAGATAACGAATGTGTGGCAGCATGGGGTTTTGTAATCACCGT 273

QY      235 TTTCACCTTCCA CTGATCTCTCGCTGGCTCAAACACACAGAGTGTGTCCATTGGACAAAC 294
DB      274 TTCACCTTGCACTGCATCAATAAATGGATCAAGACGAGAGATGCATGCCCGTTGGACAAAC 333

QY      295 AGAGATGGGNAATTCAAAAGATATGG 320
DB      334 CAACCTTGGCAATTGGCAAGGTGGCG 359

RESULT 6
US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

Query Match          39.8%; Score 130; DB 7; Length 366;
Best Local Similarity 68.0%; Pred. No. 2.6e-31;
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0

QY      55 AAGAAGCGCTTTGAAGTGA AAAAGTGGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTG 114

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Result No.	Query			ID	Description
	Score	Match	Length		
1	327	100.0	482	3	US-09-513-999C-3894
2	327	100.0	507	3	US-09-949-016-4940
3	327	100.0	508	3	US-09-914-324A-3
4	290.2	88.7	504	3	US-09-914-324A-5
5	253.6	77.6	3208	3	US-09-780-016-27
6	253.6	77.6	3208	3	US-10-214-811-27
7	253.6	77.6	3208	3	US-10-766-074-27
8	170	52.0	402	3	US-09-513-999C-10371
9	170	52.0	463	3	US-09-621-976-15180
10	153.2	46.9	411	3	US-09-640-211A-1731
11	138.2	42.3	490	3	US-09-270-767-26812
12	138.2	42.3	1101	3	US-09-270-767-11265
13	123.6	37.8	480	3	US-09-914-324A-4
14	114.4	35.0	357	3	US-09-248-796A-5495
15	92.6	28.3	25274	3	US-09-949-016-16682
16	90	27.5	301	3	US-09-313-294A-492
17	74	22.6	342	3	US-09-826-312A-7
18	74	22.6	342	3	US-09-542-497A-7
19	74	22.6	342	3	US-10-108-767-7
20	46.4	14.0	439	3	US-09-799-451-296
21	36	11.0	601	3	US-09-949-016-174803
22	33.6	10.3	87734	3	US-09-949-016-17521
23	33.4	10.2	170	3	US-09-270-767-26253
24	33.4	10.2	585	3	US-09-270-767-10788

```
|||||
Db 149 AACTGTGCCATCTGCAGGAACCAATATTGATCTTTGCATAGAAATGTCAAGTAACCAAG 208
|||
Qy 181 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
|||
Db 209 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 268
|||
Qy 241 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 300
|||
Db 269 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 328
|||
Qy 301 TGGGAATTCCAAAGATATGGCACTAG 327
|||
Db 329 TGGGAATTCCAAAGATATGGCACTAG 355
|||

RESULT 2
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4940
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4940
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Query Match 100.0%; Score 327; DB 3; Length 507;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 7 ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66
|||
Qy 61 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 120
Db 67 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 126
|||
Qy 121 AACTGTGCCATCTGCAGGAACCAATATTGATCTTTGCATAGAAATGTCAAGCTAACCAAG 180
Db 127 AACTGTGCCATCTGCAGGAACCAATATTGATCTTTGCATAGAAATGTCAAGCTAACCAAG 186
|||
Qy 181 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 187 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246
|||
Qy 241 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 300
Db 247 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 306
|||
Qy 301 TGGGAATTCCAAAGATATGGCACTAG 327
Db 307 TGGGAATTCCAAAGATATGGCACTAG 333
|||
```

```
RESULT 3
US-09-914-324A-3
; Sequence 3, Application US/09914324A
```

```
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-09-914-324A-3

Query Match 100.0%; Score 327; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 3.4e-103;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 7 ATGCGCGCAGCGATGGATGTGGATATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66
|||
Qy 61 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 120
Db 67 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 126
|||
Qy 121 AACTGTGCCATCTGCAGGAACCAATATTGATCTTTGCATAGAAATGTCAAGCTAACCAAG 180
Db 127 AACTGTGCCATCTGCAGGAACCAATATTGATCTTTGCATAGAAATGTCAAGCTAACCAAG 186
|||
Qy 181 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 187 GCGTCGCGTACTTTCAGAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246
|||
Qy 241 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 300
Db 247 TTCACATGCACTCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGACAACAGAGAG 306
|||
Qy 301 TGGGAATTCCAAAGATATGGCACTAG 327
Db 307 TGGGAATTCCAAAGATATGGCACTAG 333
|||

RESULT 4
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
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```
RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn.
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/766,074
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-074-27

Query Match 77.6%; Score 253.6; DB 3; Length 3208;
Best Local Similarity 98.5%; Pred. No. 2.6e-77; Indels 0; Gaps 0;
Matches 256; Conservative 0; Mismatches 4;

QY 68 AAGTGAAGTGAATGCAGTAGTCCCTCTGGGCGCTGGGATATTGGTTGATAACTGTG 127
Db 2765 AAAAAAAAAAATGAATGCAGTAGTCCCTCTGGGCGCTGGGATATTGGTTGATAACTGTG 2824

QY 128 CCACTGCGAGAACCACTATTATGATCTTTGGCATAGATGTCAGCTAACCGCGCTCG 187
Db 2825 CCATCTGCGAGAACCACTATTATGATCTTTGGCATAGATGTCAGCTAACCGCGCTCG 2884

QY 188 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTCACTTCCACT 247
Db 2885 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACTGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGCTCGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAAT 307
Db 2945 GCATCTCTCGCTCGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAAT 3004

QY 308 TCCAAAAGTATGGCACTAG 327
Db 3005 TCCAAAAGTATGGCACTAG 3024

RESULT 8
US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
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; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10371
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Query Match 52.0%; Score 170; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-48; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 158 GCATAGAATGTCAGCTAACCGCTGCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 217
Db 106 GCATAGAATGTCAGCTAACCGCTGCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 165

QY 218 GAGTCTGTAAACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGG 277
Db 166 GAGTCTGTAAACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGG 225

QY 278 TGTGTCCTTGGACACAGAGTGGGAATTCAAAAGTATGGGCACTAG 327
Db 226 TGTGTCCTTGGACACAGAGTGGGAATTCAAAAGTATGGGCACTAG 275

RESULT 9
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

Query Match 52.0%; Score 170; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 158 GCATAGAATGTCAGCTAACCGCTGCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 217
Db 101 GCATAGAATGTCAGCTAACCGCTGCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 160

QY 218 GAGTCTGTAAACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGG 277
Db 161 GAGTCTGTAAACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGG 220
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Qy 278 TGTGTCCATTGACAAACAGAGAGTGGGAATTCACAAAGTATGGGCACCTAG 327
 |||||
 Db 221 TGTGTCCATTGACAAACAGAGAGTGGGAATTCACAAAGTATGGGCACCTAG 270
 |||||

RESULT 10

US-09-640-211A-1731
 ; Sequence 1731, Application US/09640211A
 ; Patent No. 6833446
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Marion
 ; APPLICANT: Shenk, Michael A.
 ; APPLICANT: McGrath, Amette
 ; APPLICANT: Glenn, Matthew
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; FILE REFERENCE: Modification of Gene Transcription
 ; FILE REFERENCE: 11000.1021CIU
 ; CURRENT APPLICATION NUMBER: US/09/640,211A
 ; CURRENT FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 2368
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1731
 ; LENGTH: 411
 ; TYPE: DNA
 ; ORGANISM: Pinus radiata
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(411)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-640-211A-1731

Query Match 46.9%; Score 153.2; DB 3; Length 411;
 Best Local Similarity 77.7%; Pred. No. 7e-43;
 Matches 185; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 Qy 58 AAGCGTTTGAAGTGAAGTGAATCCAGTAGCCCTCTGGGCTGGGATATTGTGTT 117
 |||||
 Db 161 AAACGTTTCGAATCAAGAGTGAATCTGTAGCCCTTTGGCGTGGGATATTGTGTT 220
 |||||
 Qy 118 GATACTGTGCATCTGCAGAACACACATTTATGGATCTTTCATAGATGTCAAGCTAAC 177
 |||||
 Db 221 GATAATTTGCAATTTGCAGAAACACATCATGTGACCTCTGTATTAGTGTGAGCAAT 280
 |||||
 Qy 178 CAGCGTCCGCTACTTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTT 237
 |||||
 Db 281 CAAGCAAGTGAACAAAGTGAAGTGTACTGTGTGATGGGTGTTTGAATCAGCCTTT 340
 |||||
 Qy 238 CACTTCCACTGCATCTCTCGTGGCTCAAAACAGACAGGTGTGTCCATTGGACAACA 295
 |||||
 Db 341 CATTTCCATTGCATAAGTCGGTGGCTCAAGACACAGCAAGTCTGCCATTAGATAATA 398
 |||||

RESULT 11

US-09-270-767-26812/c
 ; Sequence 26812, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 26812
 ; LENGTH: 490
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-26812

Query Match 42.3%; Score 138.2; DB 3; Length 490;
 Best Local Similarity 71.0%; Pred. No. 1.2e-37;
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 49 GCGGCGAAGAGCGCTTTTGAAGTGAAGTGAATGCAGTAGGCCCTCTGGGCCCTGGGAT 108
 |||||
 Db 322 GCCAGGACGGAGCGCTTTTGTGTGAAGAAATGGGTGGCAGCCCATGTGGGGATGGGAC 263
 |||||
 Qy 109 ATTGTGTTGATAACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGT 168
 |||||
 Db 262 GTAGCAGTGGGACAACTGTGCCATCTGCCGTAAACACACATCATGAACCTGTGCATCGAGTGC 203
 |||||
 Qy 169 CAAGCTAACAGGCGTCCGTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAAC 228
 |||||
 Db 202 CAGCGGACCC---CGAATGCAAAACCAAGACGAGTGCACTGTGGCTTGGGGCGAGTGCAC 146
 |||||
 Qy 229 CATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACAGAGTGTGTCCATTG 288
 |||||
 Db 145 CACGCATTTCCATTACCACTGCATCGCGCTGGTTGAAACCGCGCTGTGTCTGTCGCGCTG 86
 |||||
 Qy 289 GACAACAGAGAGTGGGAATTCACAAAGTATGGGCACTAG 327
 |||||
 Db 85 GACAACAGAGAGTGGGTCTACCAAGAGTACGGCCGCTAG 47
 |||||

RESULT 12

US-09-270-767-11265/c
 ; Sequence 11265, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11265
 ; LENGTH: 1101
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-11265

Query Match 42.3%; Score 138.2; DB 3; Length 1101;
 Best Local Similarity 71.0%; Pred. No. 1.9e-37;
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;
 Qy 49 GCGGCGAAGAGCGCTTTTGAAGTGAAGTGAATGCAGTAGGCCCTCTGGGCCCTGGGAT 108
 |||||
 Db 933 GCCAGGACGGAGCGCTTTTGTGTGAAGAAATGGGTGGCAGCCCATGTGGGGATGGGAC 874
 |||||
 Qy 109 ATTGTGTTGATAACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGT 168
 |||||
 Db 873 GTAGCAGTGGACAACTGTGCCATCTGCCGTAAACACACATCATGAACCTGTGCATCGAGTGC 814
 |||||
 Qy 169 CAAGCTAACAGGCGTCCGTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAAC 228
 |||||
 Db 813 CAGCGGACCC---CGAATGCAAAACCAAGACGAGTGCACTGTGGCTTGGGGCGAGTGCAC 757
 |||||
 Qy 229 CATGCTTTTCACTTCCACTGCATCTCTCGTGGCTCAAAACACAGAGTGTGTCCATTG 288
 |||||
 Db 756 CACGCATTTCCATTACCACTGCATCGCGCTGGTTGAAACCGCGCTGTGTCTGTCGCGCTG 697
 |||||
 Qy 289 GACAACAGAGAGTGGGAATTCACAAAGTATGGGCACTAG 327
 |||||
 Db 696 GACAACAGAGAGTGGGTCTACCAAGAGTACGGCCGCTAG 658
 |||||

RESULT 13

US-09-914-324A-4
 ; Sequence 4, Application US/09914324A
 ; Patent No. 6858709
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Joan A.
 ; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Kamura, Takumi

